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OM protein - protein search, using sw model

Run on: February 18, 2003, 03:01:46 ; Search time 23 Seconds

(without alignments)
139.439 Million cell updates/sec

Title: US-10-033-067-1
Perfect score: 567
Sequence: 1 MKKLTPLPSKMKVSAALLCL.....ERWVRDSMKHLDQIFQNLKP 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	412	72.7	77	1	US-08-347-492B-9	Sequence 9, Appl1
2	412	72.7	77	2	US-08-421-144A-6	Sequence 6, Appl1
3	412	72.7	77	2	US-08-798-143-9	Sequence 9, Appl1
4	412	72.7	77	4	US-09-366-887A-12	Sequence 12, Appl1
5	408	72.0	76	1	US-08-480-449-20	Sequence 20, Appl1
6	408	72.0	76	2	US-08-716-188-3	Sequence 3, Appl1
7	408	72.0	76	2	US-08-660-542-20	Sequence 20, Appl1
8	408	72.0	76	4	US-08-479-603-20	Sequence 20, Appl1
9	396	69.8	74	2	US-08-615-232A-6	Sequence 6, Appl1
10	396	69.8	74	3	US-08-470-323-6	Sequence 6, Appl1
11	367	64.7	99	1	US-08-127-499A-35	Sequence 35, Appl1
12	367	64.7	99	1	US-08-482-847-35	Sequence 8, Appl1
13	367	64.7	99	1	US-08-347-492B-8	Sequence 19, Appl1
14	367	64.7	99	1	US-08-480-449-19	Sequence 5, Appl1
15	367	64.7	99	2	US-08-479-126B-5	Sequence 5, Appl1
16	367	64.7	99	2	US-08-421-144A-5	Sequence 5, Appl1
17	367	64.7	99	2	US-08-726-830A-5	Sequence 19, Appl1
18	367	64.7	99	2	US-08-660-542-19	Sequence 8, Appl1
19	367	64.7	99	2	US-08-798-143-8	Sequence 24, Appl1
20	367	64.7	99	3	US-07-927-391-24	Sequence 5, Appl1
21	367	64.7	99	3	US-08-995-156A-5	Sequence 5, Appl1
22	367	64.7	99	3	US-09-044-856A-5	Sequence 5, Appl1
23	367	64.7	99	3	US-09-044-855A-5	Sequence 152, App
24	367	64.7	99	4	US-08-679-493A-152	Sequence 19, Appl1
25	367	64.7	99	4	US-08-479-603-19	Sequence 5, Appl1
26	367	64.7	99	4	US-09-419-281-5	Sequence 10, Appl1
27	367	64.7	99	4	US-09-366-887A-10	

28	367	64.7	99	5	PCT-US96-10087-5
29	367	64.7	99	6	5212073-2
30	357	63.0	109	2	US-08-421-144A-7
31	357	63.0	109	3	US-07-927-391-16
32	357	63.0	109	4	US-08-679-493A-153
33	354	62.4	110	4	US-09-366-887A-13
34	350	61.7	97	4	US-09-366-887A-27
35	337	59.4	99	1	US-08-480-449-18
36	337	59.4	99	2	US-08-660-542-18
37	337	59.4	99	4	US-08-613-822-18
38	337	59.4	99	4	US-08-479-603-18
39	337	59.4	99	4	US-08-479-729B-18
40	334.5	59.0	96	4	US-09-230-637-44
41	328.5	57.9	98	4	US-08-613-822-4
42	328.5	57.9	98	4	US-08-852-212-2
43	328.5	57.9	98	4	US-09-479-729B-4
44	328.5	57.9	98	4	US-09-261-201A-4
45	319.5	56.3	104	4	US-08-744-419-2

ALIGNMENTS

Sequence 5, Appl1
Patent No. 5212073
Sequence 7, Appl1
Sequence 16, Appl1
Sequence 153, App
Sequence 17, Appl1
Sequence 27, Appl1
Sequence 18, Appl1
Sequence 18, Appl1
Sequence 18, Appl1
Sequence 4, Appl1
Sequence 44, Appl1
Sequence 2, Appl1
Sequence 4, Appl1
Sequence 4, Appl1
Sequence 2, Appl1

RESULT 1
US-08-347-492B-9
; Sequence 9, Application US/08347492B
; Patent No. 5602008
; GENERAL INFORMATION:
; APPLICANT: Wilde, Craig G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,492B
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,241
; FILING DATE: 07-SEP-1994
; APPLICATION NUMBER: 08/320,011
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI 126829
; US-08-347-492B-9

Query Match 72.7%; Score 412; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6e-45;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AQPDSVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 92
Db 1 AQPDSVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60

QY 93 VRDSMKHLDQIFQNLKP 109
Db 61 VRDSMKHLDQIFQNLKP 77

RESULT 2

US-08-421-144A-6
; Sequence 6, Application US/08421144A
; Patent No. 5874211

GENERAL INFORMATION:

APPLICANT: BANDMAN, OLGA
APPLICANT: COLEMAN, ROGER
APPLICANT: STUART, SUSAN G.
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,144A
FILING DATE: 13-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF-0031 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-421-144A-6

Query Match 72.7%; Score 412; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6e-45;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AQPDSVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 92
Db 1 AQPDSVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60

QY 93 VRDSMKHLDQIFQNLKP 109
Db 61 VRDSMKHLDQIFQNLKP 77

RESULT 3
US-08-798-143-9
; Sequence 9, Application US/08798143
; Patent No. 5936068

GENERAL INFORMATION:

APPLICANT: Wilde, Craig G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
TITLE OF INVENTION: PRODUCTION AND USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,143
FILING DATE: 10-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,492
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: 08/303,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 126829

US-08-798-143-9

Query Match 72.7%; Score 412; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6e-45;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AQPDSVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 92
Db 1 AQPDSVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60

QY 93 VRDSMKHLDQIFQNLKP 109
Db 61 VRDSMKHLDQIFQNLKP 77

RESULT 4

US-09-366-887A-12
; Sequence 12, Application US/09366887A
; Patent No. 6403782

GENERAL INFORMATION:

APPLICANT: LUSTER, ANDREW D.
APPLICANT: LEDER, PHILIP
APPLICANT: ROTHENBERG, MARC
APPLICANT: GARCIA, EDUARDO
TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT

FILE REFERENCE: 00383/025002
CURRENT APPLICATION NUMBER: US/09/366,887A
CURRENT FILING DATE: 1999-08-04
PRIOR APPLICATION NUMBER: 60/000,449
PRIOR FILING DATE: 1995-06-22
PRIOR APPLICATION NUMBER: 08/522,713
PRIOR FILING DATE: 1995-09-01
PRIOR APPLICATION NUMBER: 08/522,713
PRIOR FILING DATE: 1998-06-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
US-09-366-887A-12

Query Match 72.7%; Score 412; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6e-45;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AQPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 92
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Db 1 AQPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60

QY 93 VRDSMKHLDQIFONLKP 109
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Db 61 VRDSMKHLDQIFONLKP 77

RESULT 5

US-08-480-449-20
Sequence 20, Application US/08480449
Patent No. 5688927
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,449
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27866/32779
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "Hu MCP-2"

US-08-480-449-20

Query Match 72.0%; Score 408; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 93
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Db 1 QPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60

QY 94 RDSMKHLDQIFONLKP 109
|||||
Db 61 RDSMKHLDQIFONLKP 76

RESULT 6

US-08-716-188-3
Sequence 3, Application US/08716188
Patent No. 5908829
GENERAL INFORMATION:
APPLICANT: KELLY, RODNEY W
TITLE OF INVENTION: USE OF MCP-1 FOR INDUCING RIPENING OF
TITLE OF INVENTION: THE CERVIX
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,188
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00733
FILING DATE: 31-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9406463.1
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-219
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-716-188-3

Query Match 72.0%; Score 408; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 93
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Db 1 QPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60

QY 94 RDSMKHLDQIFONLKP 109
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Db 61 RDSMKHLDQIFONLKP 76

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RESULT 7
US-08-660-542-20
; Sequence 20, Application US/08660542
; Patent No. 5932703
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,542
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,658
; FILING DATE: 16-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,620
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/33318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "Hu MCP-2"
US-08-660-542-20

Query Match          72.0%; Score 408; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 34 QPDSVSIPTCCFNVINRKIPQRLSYTRITNIQCPKEAVIFKTRGKEVCADPKERWV 93
DB 1 QPDSVSIPTCCFNVINRKIPQRLSYTRITNIQCPKEAVIFKTRGKEVCADPKERWV 60

OY 94 RDSMKHLDQIFQNLKP 109
DB 61 RDSMKHLDQIFQNLKP 76
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RESULT 8
US-08-479-603-20
; Sequence 20, Application US/08479603
; Patent No. 6320023
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
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; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,603
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/32780
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "Hu MCP-2"
US-08-479-603-20

Query Match          72.0%; Score 408; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 34 QPDSVSIPTCCFNVINRKIPQRLSYTRITNIQCPKEAVIFKTRGKEVCADPKERWV 93
DB 1 QPDSVSIPTCCFNVINRKIPQRLSYTRITNIQCPKEAVIFKTRGKEVCADPKERWV 60

OY 94 RDSMKHLDQIFQNLKP 109
DB 61 RDSMKHLDQIFQNLKP 76
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RESULT 9
US-08-615-232A-6
; Sequence 6, Application US/08615232A
; Patent No. 5993814
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,232A
FILING DATE: 13-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9318984
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: GB 9408602
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 550-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-615-232A-6

Query Match 69.8%; Score 396; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.5e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 DVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKVCADPKERWVRD 95
|||||
Db 1 DVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKVCADPKERWVRD 60

QY 96 SMKHLDOI FQNLKP 109
|||||
Db 61 SMKHLDOI FQNLKP 74

RESULT 10
US-08-470-323-6
Sequence 6, Application US/08470323A
Patent No. 6031080
GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
APPLICANT: HSUAN, JOHN J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
FILE REFERENCE: 550-33
CURRENT APPLICATION NUMBER: US/08/470,323A
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: PCT/GB94/02006
EARLIER FILING DATE: 1994-09-14
EARLIER APPLICATION NUMBER: GB 9318984.3
EARLIER FILING DATE: 1993-09-14
EARLIER APPLICATION NUMBER: GB 94086902.2
EARLIER FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 6
LENGTH: 74
TYPE: PRT
ORGANISM: human
US-08-470-323-6

Query Match 69.8%; Score 396; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.5e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 DVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKVCADPKERWVRD 95
|||||
Db 1 DVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKVCADPKERWVRD 60

QY 96 SMKHLDOI FQNLKP 109
|||||
Db 61 SMKHLDOI FQNLKP 74

RESULT 11
US-08-127-499A-35
Sequence 35, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-35

Query Match 64.7%; Score 367; DB 1; Length 99;
Best Local Similarity 69.4%; Pred. No. 6.4e-39;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 11 MKVSALLCLLMAATFSPQGLAQPDVSIPITCCFNVINRKIPQRLSEYTRITNIQCP 70
|||||
Db 1 MKVSALLCLLMAATFIPQGLAQPDAINAPVTCYNTNRKISVQRLASRYRTSSKCP 60

QY 71 KEAVIFKTKRGKVCADPKERWVRDSMKHLDOI FQNLK 108
|||||
Db 61 KEAVIFKTIKVCADPKQKQVODSMHDLKQOTQTPK 98

RESULT 12
US-08-482-847-35
Sequence 35, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-35

Query Match 64.7%; Score 367; DB 1; Length 99;
Best Local Similarity 69.4%; Pred. No. 6.4e-39;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

OY 11 MKVSALLCLLMAATFSPQGLAOPDSVIPITCCFNVINRKIPQRLSYRTITNIQCP 70
|||||
Db 1 MKVSALLCLLIIATFIPQGLAOPDAINAPVTCYNTNRKISVQRLASYRRITSSKCP 60

OY 71 KEAVIFKTRGKEVCADPKERWVDSMKHLDOI FQNLK 108
|||||
Db 61 KEAVIFKTVAKEICADPKQKWQDSMDHLDKQTQTPK 98

RESULT 13
US-08-347-492B-8
Sequence 8, Application US/08347492B
Patent No. 5602008
GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Selthamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
TITLE OF INVENTION: PRODUCTION AND USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,492B
FILING DATE: 29-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 487124
US-08-347-492B-8

Query Match 64.7%; Score 367; DB 1; Length 99;
Best Local Similarity 69.4%; Pred. No. 6.4e-39;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

OY 11 MKVSALLCLLMAATFSPQGLAOPDSVIPITCCFNVINRKIPQRLSYRTITNIQCP 70
|||||
Db 1 MKVSALLCLLIIATFIPQGLAOPDAINAPVTCYNTNRKISVQRLASYRRITSSKCP 60

OY 71 KEAVIFKTRGKEVCADPKERWVDSMKHLDOI FQNLK 108
|||||
Db 61 KEAVIFKTVAKEICADPKQKWQDSMDHLDKQTQTPK 98

RESULT 14
US-08-480-449-19
Sequence 19, Application US/08480449
Patent No. 5688927
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,449
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27866/32779
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "Hu MCP-1"
US-08-480-449-19

Query Match 64.7%; Score 367; DB 1; Length 99;
Best Local Similarity 69.4%; Pred. No. 6.4e-39;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 11 MKVSALLCLLLMAATFSPQGLAQPDSVSIPITCCFNVINRKIPQRLSEYTRITNIQCP 70
|||||
Db 1 MKVSALLCLLLIAATFIPQGLAQPDAINAPVTCCTCYNFTNRKISVQRLASYRRITSSKCP 60

QY 71 KEAVIFKTRKGKVCADPKERWVRDSMKHLDOIIFQNLK 108
|||||
Db 61 KEAVIFKTIIVAKEICADPKQKWVQDSMDHLDKQTQTPK 98

RESULT 15

US-08-479-126B-5
Sequence 5, Application US/08479126B
Patent No. 5866373

GENERAL INFORMATION:

APPLICANT: LI, HAODONG
APPLICANT: RUBEN, STEVEN M
APPLICANT: SUTON, GRANGER G III
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN MONOCYTE
TITLE OF INVENTION: CHEMOTACTIC PROTEIN-4 (AS AMENDED)
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC

COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,126B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0340001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 99 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-479-126B-5

Search completed: February 18, 2003, 03:06:35
Job time : 24 secs

QY 11 MKVSALLCLLLMAATFSPQGLAQPDSVSIPITCCFNVINRKIPQRLSEYTRITNIQCP 70
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Db 1 MKVSALLCLLLIAATFIPQGLAQPDAINAPVTCCTCYNFTNRKISVQRLASYRRITSSKCP 60

QY 71 KEAVIFKTRKGKVCADPKERWVRDSMKHLDOIIFQNLK 108
|||||
Db 61 KEAVIFKTIIVAKEICADPKQKWVQDSMDHLDKQTQTPK 98

Query Match 64.7%; Score 367; DB 2; Length 99;
Best Local Similarity 69.4%; Pred. No. 6.4e-39;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: February 18, 2003, 01:56:46 ; Search time 70 Seconds

(without alignments)
207.490 Million cell updates/sec

Title: US-10-033-067-1

Perfect score: 567
Sequence: 1 MLKLTPLPSKMKVSALLCL.....ERWVRDSMKHLDQIFQNLKP 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
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23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	567	100.0	109	19	AAW42072	Human MC proprotel
2	567	100.0	109	23	ABG35167	Reference sequence
3	563	99.3	109	18	AAW26655	Human beta-chemoki
4	563	99.3	109	23	ABG35168	Polymorphic varian
5	562	99.1	109	23	ABG35169	Polymorphic varian
6	517	91.2	99	20	AAV05300	C-C Chemokine, MCP
7	517	91.2	99	20	AAV07233	Wild type monocyte
8	517	91.2	99	20	AAV07237	Wild type monocyte
9	412	72.7	77	21	AAB15786	Human chemokine MC
10	412	72.7	77	23	ABB80903	Human MCP2 fragmen

11	408	72.0	76	21	AAV69031	Amino acid sequenc
12	408	72.0	76	23	AAO21099	protein of WT-MCP-
13	408	72.0	76	23	AAO21109	MCP-2 chemokine pr
14	404	71.3	76	23	AAV78390	Human chemokine hm
15	404	71.3	76	23	AAV68353	Human monocyte che
16	389	68.6	77	20	AAV14223	Chemokine hMCP2.
17	382	67.4	71	20	AAV07234	Truncated monocyte
18	382	67.4	71	20	AAV07238	Truncated monocyte
19	367	64.7	99	13	AAV28663	MCF. Synthetic.
20	367	64.7	99	16	AAV73914	Human monocyte che
21	367	64.7	99	16	AAV70800	Chemottractant pr
22	367	64.7	99	19	AAV40174	Macrophage chemoa
23	367	64.7	99	20	AAV48391	Human prostate can
24	367	64.7	99	20	AAV26176	Monocyte chemoa
25	367	64.7	99	21	AAB15785	Human chemokine MC
26	367	64.7	99	22	AAB97914	Human monocyte che
27	367	64.7	99	23	AAV77179	Human MCP1 fragmen
28	367	64.7	99	23	AAV52440	HIV_Nef1 fusion pr
29	367	64.7	99	23	AAV95387	Human small induci
30	363	64.0	99	10	AAV06398	Human monocyte che
31	363	64.0	99	11	AAV06398	Human MCF precurs
32	360.5	63.6	77	23	AAV78395	Mouse/human hybrid
33	360.5	63.6	77	23	AAV68358	Chemottractant MC
34	358	63.1	72	16	AAV70804	Chemottractant MC
35	357	63.0	109	13	AAV24353	Cytokine encoded b
36	357	63.0	109	22	AAV27814	Full-length polype
37	357	63.0	109	23	AAO21490	Small inducible cy
38	357	63.0	109	23	AAV52441	HIV_Nef1 fusion pr
39	357	63.0	143	22	AAO12965	Human polypeptide
40	354	62.4	94	23	AAV78393	Mouse/human hybrid
41	354	62.4	94	23	AAV68356	Chimeric chemokine
42	354	62.4	110	23	ABB80904	Human MCP3 fragmen
43	350	61.7	97	18	AAV14990	Human eosinocyte C
44	350	61.7	97	18	AAV10099	Human eotaxin. Ho
45	350	61.7	97	21	AAB15794	Human chemokine eo

ALIGNMENTS

RESULT 1	
AAW42072	standard; Protein; 109 AA.
ID	AAW42072
XX	
AC	AAW42072;
XX	
DT	09-JUN-1998 (first entry)
XX	
DE	Human MC proprotein.
XX	
KW	Human monocyte chemotactic proprotein; MCP; incyte clone; allergy;
KW	macrophage; diagnostic assay; body fluid; lung; biopsy;
KW	autoimmune disease; AIDS; asthma; rheumatoid arthritis; NIDDM;
KW	breast cancer; bladder.
XX	
OS	Homo sapiens.
XX	
PN	WO9802459-A1.
XX	
PD	22-JAN-1998.
XX	
PF	15-JUL-1997; 97WO-US12349.
XX	
PR	15-JUL-1996; 96US-0683655.
XX	
PA	(INCY-) INCYTE PHARM INC.
XX	
PI	Au-Young J, Coleman R, Hillman JL;
XX	
DR	WPI; 1998-110529/10.
DR	N-PSDB; AAV09218.
XX	
PT	New human monocyte chemotactic proprotein - has homology to CC

PF chemokine(s) useful for identifying agent for treating auto-immune
PT diseases or allergic responses
XX
PS Claim 1; Pages 38-39; 53pp; English.
XX
CC The is a human monocyte chemotactic proprotein sequence. Its cDNA was
CC first identified in incyte clone 965517 from a breast cDNA library.
CC Antisense nucleotides can be used to control human MCPP expression
CC especially where it may lead to inappropriate monocyte or macrophage
CC activity causing damage associated with allergic responses to organs
CC such as the lungs. Antisense nucleotides and MCPP cDNA may be used
CC in diagnostic assays of body fluids or biopsied tissues to detect
CC expression levels of MCPP. MCPP cDNA may also be useful for
CC treatment of disorders such as asthma, rheumatoid arthritis, NIDDM
CC or cancer of the breast or bladder. Human MCPP protein can be used to
CC identify agonists, antagonists or inhibitors to modulate the activity of
CC MCPP in allergic responses or autoimmune diseases such as AIDS.
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 567; DB 19; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKLTPLPSKMKVSALLCLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPQRLS 60
DB 1 MLKLTPLPSKMKVSALLCLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPQRLS 60

QY 61 YTRITNIQCPKEAVIFKTRGKEVCADPKERWVDSMKHLDOI FQNLKP 109
DB 61 YTRITNIQCPKEAVIFKTRGKEVCADPKERWVDSMKHLDOI FQNLKP 109

RESULT 2
ABG35167
ID ABG35167 standard; Protein; 109 AA.
XX
AC ABG35167;
XX
DT 15-JUL-2002 (first entry)
XX
DE Reference sequence for human SCYA8 polypeptide.
XX
KW Human; single nucleotide polymorphism; SNP; monocyte chemotactic protein;
KW small inducible cytokine subfamily A member 8; SCYA8; antiinflammatory;
KW haplotyping; genotyping; inflammatory disease; HIV infection;
KW human immunodeficiency virus; anti-HIV.
XX
OS Homo sapiens.
XX
PN WO200222888-A1.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US29332.
XX
PR 15-SEP-2000; 2000US-232755P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Chew A, Han J, Lee HH;
XX
DR WPI; 2002-371973/40.
DR N-PSDB; ABR70707.
XX
PT New genetic variants of Small Inducible Cytokine Subfamily A (Cys-Cys),
PT Member 8 (Monocyte Chemotactic protein) isogenes, useful for improving
PT efficiency and reliability in drug development for treating diseases
XX
PS Claim 29; Fig 3; 84pp; English.
XX
CC The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human small inducible cytokine subfamily A (Cys-Cys),

CC member 8 (monocyte chemotactic protein) (SCYA8) gene located on
CC chromosome 17, and methods for haplotyping and/or genotyping the SCYA8
CC gene. The methods of the invention make use of allele-specific
CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
CC oligonucleotides for detecting the SCYA8 gene polymorphisms. The
CC polynucleotides and screened compounds are useful for the treatment of
CC diseases associated with SCYA8 activity, such as inflammatory diseases
CC and human immunodeficiency virus (HIV) infection. The present sequence
CC represents a reference sequence for the human SCYA8 polypeptide.
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 567; DB 23; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKLTPLPSKMKVSALLCLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPQRLS 60
DB 1 MLKLTPLPSKMKVSALLCLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPQRLS 60

QY 61 YTRITNIQCPKEAVIFKTRGKEVCADPKERWVDSMKHLDOI FQNLKP 109
DB 61 YTRITNIQCPKEAVIFKTRGKEVCADPKERWVDSMKHLDOI FQNLKP 109

RESULT 3
AAW26655
ID AAW26655 standard; Protein; 109 AA.
XX
AC AAW26655;
XX
DT 16-FEB-1998 (first entry)
XX
DE Human beta-chemokine H1305 (MCP-2).
XX
KW H1305; MCP-2; chemokine; human; chemoattractant; chemotaxis;
KW virus infection; HIV; therapy; wound healing; tumour; antibody.
XX
OS Homo sapiens.
XX
PN WO9725427-A1.
XX
PD 17-JUL-1997.
XX
PF 10-JAN-1997; 97WO-US00379.
XX
PR 12-JAN-1996; 96US-0586395.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Lavallie ER, McCoy JM, Racie LA;
XX
DR WPI; 1997-372866/34.
DR N-PSDB; AAT91023.
XX
PT New human beta-chemokine, H1305 and corresponding DNA - used in the
PT treatment of viral infection, e.g. HIV, and in wound healing
XX
PS Claim 1; Page 12-13; 21pp; English.
XX
CC This protein comprises human beta-chemokine H1305, also known as
CC MCP-2. Its sequence was deduced from a claimed cDNA clone (see
CC AAT91023) isolated from a human peripheral blood mononuclear cell
CC cDNA library. Also claimed are: (1) a host cell, preferably
CC mammalian, transformed with a H1306 polynucleotide operably linked
CC to an expression control sequence; (2) a recombinantly produced
CC H1305 protein; and (3) a composition comprising an antibody which
CC specifically reacts with the H1305 protein. The H1305 protein
CC may be used in a composition for the treatment of a mammalian
CC subject (claimed). It is thought to have chemokine activities and
CC may therefore have an effect on chemotaxis or migration of blood
CC cells. It may be useful for inhibiting viral replication, including
CC replication of HIV, and may also be used for treatment of

CC wounds and to raise monoclonal and polyclonal antibodies which
CC specifically react with H1305. Such antibodies may be used for
CC therapy of certain tumours as they are capable of blocking the
CC ligand binding of the H1305 protein or may promote clearance of
CC the protein from the patient.

XX SQ Sequence 109 AA;

Query Match 99.3%; Score 563; DB 18; Length 109;
Best Local Similarity 99.1%; Pred. No. 7.4e-59;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKLTPLPSKMKVSAALLCLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIQRLS 60
|||||
Db 1 MLKLTPLPSKMKVSAALLCLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIQRLS 60

QY 61 YTRITNIQCPKEAVIFKTRGKEVCADPKERWVRDSMKHLDQIFQNLKP 109
|||||
Db 61 YTRITNIQCPKEAVIFKTRGKEVCADPKERWVRDSMKHLDQIFQNLKP 109

RESULT 4
ABG35168

ID ABG35168 standard; Protein; 109 AA.

XX AC ABG35168;

DT 15-JUL-2002 (first entry)

DE Polymorphic variant #1 of human SCYA8 polypeptide.

XX KW Human; single nucleotide polymorphism; SNP; monocyte chemotactic protein;
KW small inducible cytokine subfamily A member 8; SCYA8; antiinflammatory;
KW haplotyping; genotyping; inflammatory disease; HIV infection;
KW human immunodeficiency virus; anti-HIV.

XX OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 79 /note= "Substitution of Lys to Gln"

FT WO200222888-A1.

XX PD 21-MAR-2002.

XX PF 17-SEP-2001; 2001WO-US29332.

XX PR 15-SEP-2000; 2000US-232755P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Anastasio AE, Chew A, Han J, Lee HH;

XX DR WPI; 2002-371973/40.

XX PT New genetic variants of Small Inducible Cytokine Subfamily A (Cys-Cys),
PT Member 8 (Monocyte Chemotactic protein) isogenes, useful for improving
PT efficiency and reliability in drug development for treating diseases

XX PS Claim 29; Page -: 84pp; English.

XX CC The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human small inducible cytokine subfamily A (Cys-Cys),
CC member 8 (monocyte chemotactic protein) (SCYA8) gene located on
CC chromosome 17, and methods for haplotyping and/or genotyping the SCYA8
CC gene. The methods of the invention make use of allele-specific
CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
CC oligonucleotides for detecting the SCYA8 gene polymorphisms. The
CC polynucleotides and screened compounds are useful for the treatment of
CC diseases associated with SCYA8 activity, such as inflammatory diseases
CC and human immunodeficiency virus (HIV) infection. The present sequence
CC represents a polymorphic variant of the human SCYA8 polypeptide

CC (ABG35167).
CC Note: The present sequence is not given in the specification but is
CC created by the indexer from the information given in fig. 3 of the
CC patent.

XX SQ Sequence 109 AA;

Query Match 99.3%; Score 563; DB 23; Length 109;
Best Local Similarity 99.1%; Pred. No. 7.4e-59;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKLTPLPSKMKVSAALLCLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIQRLS 60
|||||
Db 1 MLKLTPLPSKMKVSAALLCLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIQRLS 60

QY 61 YTRITNIQCPKEAVIFKTRGKEVCADPKERWVRDSMKHLDQIFQNLKP 109
|||||
Db 61 YTRITNIQCPKEAVIFKTRGKEVCADPKERWVRDSMKHLDQIFQNLKP 109

RESULT 5
ABG35169

ID ABG35169 standard; Protein; 109 AA.

XX AC ABG35169;

DT 15-JUL-2002 (first entry)

DE Polymorphic variant #2 of human SCYA8 polypeptide.

XX KW Human; single nucleotide polymorphism; SNP; monocyte chemotactic protein;
KW small inducible cytokine subfamily A member 8; SCYA8; antiinflammatory;
KW haplotyping; genotyping; inflammatory disease; HIV infection;
KW human immunodeficiency virus; anti-HIV.

XX OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 84 /note= "Substitution of Val to Phe"

FT WO200222888-A1.

XX PD 21-MAR-2002.

XX PF 17-SEP-2001; 2001WO-US29332.

XX PR 15-SEP-2000; 2000US-232755P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Anastasio AE, Chew A, Han J, Lee HH;

XX DR WPI; 2002-371973/40.

XX PT New genetic variants of Small Inducible Cytokine Subfamily A (Cys-Cys),
PT Member 8 (Monocyte Chemotactic protein) isogenes, useful for improving
PT efficiency and reliability in drug development for treating diseases

XX PS Claim 29; Page -: 84pp; English.

XX CC The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human small inducible cytokine subfamily A (Cys-Cys),
CC member 8 (monocyte chemotactic protein) (SCYA8) gene located on
CC chromosome 17, and methods for haplotyping and/or genotyping the SCYA8
CC gene. The methods of the invention make use of allele-specific
CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
CC oligonucleotides for detecting the SCYA8 gene polymorphisms. The
CC polynucleotides and screened compounds are useful for the treatment of
CC diseases associated with SCYA8 activity, such as inflammatory diseases
CC and human immunodeficiency virus (HIV) infection. The present sequence
CC represents a polymorphic variant of the human SCYA8 polypeptide
(ABG35167).

CC Note: The present sequence is not given in the specification but is
CC created by the indexer from the information given in fig. 3 of the
CC patent.

XX Sequence 109 AA;

Query Match 99.1%; Score 562; DB 23; Length 109;
Best Local Similarity 99.1%; Pred. No. 9.7e-59;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLKLTPLPSKMKVSALLCLLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIORLES 60
Db 1 MLKLTPLPSKMKVSALLCLLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIORLES 60

OY 61 YTRITNIQCPKEAVIFKTRGKEVCADPKERWVRDSMKHLDQIFONLKP 109
Db 61 YTRITNIQCPKEAVIFKTRGKEVCADPKERWVRDSMKHLDQIFONLKP 109

RESULT 6
AAV05300

ID AAY05300 standard; protein; 99 AA.

XX AAY05300;

DT 25-JUN-1999 (first entry)

DE C-C chemokine, MCP2.

KW C-C chemokine; RANTES; MCP2; chemokine antagonist; inflammatory disease;
KW HIV infection; tumour; angiogenesis-related disease; autoimmune disease;
KW haematopoiesis-related disease; CD26/DP IV; immune disease; diagnosis;
KW atherosclerosis; pulmonary disease; skin disorder; therapy.

OS Homo sapiens.

PN EP905240-A1.

PD 31-MAR-1999.

PF 19-DEC-1997; 97EP-0122471.

PR 29-SEP-1997; 97EP-0116863.

PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PI Proost P, Struyf S, Van Damme J;

DR WPI; 1999-216695/19.

PT New amino-terminally truncated C-C chemokines have antagonistic
PT activity, for treatment of immune, inflammatory and infectious
PT diseases

PS Claim 4; Fig 1; 30pp; English.

XX This sequence represents the C-C chemokine MCP2. The invention relates
CC to amino-terminally truncated C-C chemokines, having chemokine
CC antagonistic activity. The truncated chemokines are specifically
CC residues 26 to 91 of the RANTES sequence (see AAY05299) or residues 29 to
CC 99 of the MCP2 sequence (this sequence). The new chemokines are useful
CC as medicaments, for diagnosis and/or treatment of diseases which require
CC antagonistic activity of a chemokine e.g. inflammatory diseases, HIV
CC infection, tumours, and angiogenesis- and haematopoiesis-related
CC diseases. The invention also relates to the use of CD26/DP IV for
CC treatment of inflammatory, immune and infectious diseases, including
CC autoimmune diseases, atherosclerosis, pulmonary diseases and skin
CC disorders.

XX Sequence 99 AA;

Query Match 91.2%; Score 517; DB 20; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.9e-53;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 MKVSALLCLLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIORLESYTRITNIQCP 70
Db 1 MKVSALLCLLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIORLESYTRITNIQCP 60

OY 71 KEAVIFKTRGKEVCADPKERWVRDSMKHLDQIFONLKP 109
Db 61 KEAVIFKTRGKEVCADPKERWVRDSMKHLDQIFONLKP 99

RESULT 7
AAY07233

ID AAY07233 standard; protein; 99 AA.

XX AAY07233;

DT 06-JUL-1999 (first entry)

DE Wild type monocyte chemotactic protein 2.

KW Wild type; C-C chemokine; monocyte chemotactic protein 2; MCP2; HIV;
KW regulated on activation normal T-cell expressed and secreted; RANTES;
KW truncation; antagonist; medicaments; diagnosis; inflammation; infection;
KW tumour; angiogenesis; hematopoiesis; autoimmune disease; atherosclerosis;
KW pulmonary disease; skin disorder.

OS Homo sapiens.

PN EP906954-A1.

PD 07-APR-1999.

PF 29-SEP-1997; 97EP-0116863.

PR 29-SEP-1997; 97EP-0116863.

PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PI Proost P, Struyf S, Van Damme J;

DR WPI; 1999-207108/18.

PT New amino-terminally truncated C-C chemokines have antagonistic
PT activity for treatment of immune, inflammatory and infectious
PT diseases

PS Disclosure; Fig 1; 29pp; English.

XX This sequence represents the wild type C-C chemokine monocyte chemotactic
CC protein 2 (MCP2). The invention relates the generation of amino-terminal
CC truncated C-C chemokines, having chemokine antagonistic activity. The
CC new chemokines are useful as medicaments, for diagnosis and/or treatment
CC of diseases which require antagonistic activity of a chemokine e.g.
CC inflammatory diseases, HIV infection, tumours, and angiogenesis- and
CC hematopoiesis-related diseases, including auto-immune diseases,
CC atherosclerosis, pulmonary diseases and skin disorders.

XX Sequence 99 AA;

Query Match 91.2%; Score 517; DB 20; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.9e-53;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 MKVSALLCLLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIORLESYTRITNIQCP 70
Db 1 MKVSALLCLLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIORLESYTRITNIQCP 60

OY 71 KEAVIFKTRGKEVCADPKERWVRDSMKHLDQIFONLKP 109
Db 61 KEAVIFKTRGKEVCADPKERWVRDSMKHLDQIFONLKP 99

```
RESULT 8
AAy07237
ID  AAy07237 standard; protein; 99 AA.
XX
AC  AAy07237;
XX
DT  06-JUL-1999 (first entry)
XX
DE  Wild type monocyte chemotactic protein 2.
XX
KW  Wild type; C-C chemokine; monocyte chemotactic protein 2; MCP2; HIV;
KW  regulated on activation normal T-cell expressed and secreted; RANTES;
KW  truncation; antagonist; medicaments; diagnosis; inflammation; infection;
KW  tumour; angiogenesis; hematopoiesis; autoimmune disease; atherosclerosis;
KW  pulmonary disease; skin disorder.
XX
OS  Homo sapiens.
XX
PN  EP905241-A1.
XX
PD  31-MAR-1999.
XX
PF  10-MAR-1998; 98EP-0104216.
XX
PR  19-DEC-1997; 97EP-0122471.
PR  29-SEP-1997; 97EP-0116863.
XX
PA  (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI  Proost P, Struyf S, Van Damme J;
XX
DR  WPI; 1999-206774/18.
XX
PT  New amino-terminally truncated C-C chemokines have antagonistic
PT  activity for treatment of immune, inflammatory and infectious
PT  diseases
XX
PS  Disclosure; Fig 1; 36pp; English.
XX
CC  This sequence represents the wild type C-C chemokine monocyte chemotactic
CC  protein 2 (MCP2). The invention relates the generation of amino-terminal
CC  truncated C-C chemokines, having chemokine antagonistic activity. The
CC  new chemokines are useful as medicaments, for diagnosis and/or treatment
CC  of diseases which require antagonistic activity of a chemokine e.g.
CC  inflammatory diseases, HIV infection, tumours, and angiogenesis- and
CC  hematopoiesis-related diseases, including auto-immune diseases,
CC  atherosclerosis, pulmonary diseases and skin disorders.
XX
SQ  Sequence 99 AA;

Query Match          91.2%; Score 517; DB 20; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.9e-53;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  11 MKVSALLCLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIQRLSYTRITNIQCP 70
    |||||||
DB  1 MKVSALLCLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIQRLSYTRITNIQCP 60
QY  71 KEAVIFKTRGKEVCADPKERVRVDSMKHLDFQNLKP 109
    |||||||
DB  61 KEAVIFKTRGKEVCADPKERVRVDSMKHLDFQNLKP 99
```

```
RESULT 9
AAB15786
ID  AAB15786 standard; Protein; 77 AA.
XX
AC  AAB15786;
XX
DT  17-JAN-2001 (first entry)
XX
DE  Human chemokine MCP-2 SEQ ID NO: 17.
XX
```

```
KW  Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
KW  monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
KW  AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
KW  basophil-mediated disease; myocardial infarction; acute ischaemia;
KW  rheumatoid arthritis; contraception.
XX
OS  Homo sapiens.
XX
FH  key Location/Qualifiers
FT  Misc-difference 47 /note= "encoded by CAA"
FT  WO200042071-A2.
XX
PD  20-JUL-2000.
XX
PF  12-JAN-2000; 2000WO-US00821.
XX
PR  12-JAN-1999; 99US-0229071.
PR  17-MAR-1999; 99US-0271192.
PR  01-DEC-1999; 99US-0452406.
XX
PA  (NEOR-) NEORX CORP.
XX
PI  Grainger DJ, Tatalick LM;
XX
DR  WPI; 2000-499101/44.
DR  N-PSDB; AAA74886.
XX
PT  New peptide 3, amide and heterocyclic compounds and saccharide
PT  conjugates used for inhibiting chemokine induced activity and for
PT  treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
PT  growth
XX
XX  Example 1; Page 134; 387pp; English.
XX
PS  The present invention concerns the identification of a number of
CC  chemokines which can be used to produce derivatives, agonists and
CC  antagonists which are then useful in disease treatment. The chemokines
CC  include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
CC  These chemokine derivatives can be used to treat diseases such as
CC  autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
CC  AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
CC  diseases, endotoxaemia, myocardial infarction, acute ischaemia and
CC  rheumatoid arthritis, and can be used to prevent strokes and as
CC  contraceptives. The coding sequences for the chemokines can be used in
CC  gene therapy for the same diseases, as well as in the production of
CC  animal models.
XX
SQ  Sequence 77 AA;

Query Match          72.7%; Score 412; DB 21; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.8e-41;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  33 AQPDSVSIPITCCFNVINRKIPIQRLSYTRITNIQCPKEAVIFKTRGKEVCADPKERW 92
    |||||||
DB  1 AQPDSVSIPITCCFNVINRKIPIQRLSYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60
QY  93 VRDSMKHLDFQNLKP 109
    |||||||
DB  61 VRDSMKHLDFQNLKP 77
```

```
RESULT 10
ABB80903
ID  ABB80903 standard; Protein; 77 AA.
XX
AC  ABB80903;
XX
DT  08-OCT-2002 (first entry)
XX
DE  Human MCP2 fragment.
XX
```


XX Eotaxin; eosinophil; chemotaxis; cytostatic; antiinflammatory; cardiant;
KW antiallergic; immunosuppressive; antiasthmatic; antiparasitic; histamine;
KW dermatological; vasotropic; monocyte chemoattractive protein; MCP;
KW gene therapy; antianaphylactic.
XX
OS Homo sapiens.
XX
PN US6403782-B1.
XX
PD 11-JUN-2002.
XX
PF 04-AUG-1999; 99US-0366887.
XX
PR 22-JUN-1995; 95US-000449P.
PR 01-SEP-1995; 95US-0522713.
XX
PA (HARD) HARVARD COLLEGE.
XX (GEHO) GEN HOSPITAL CORP.
XX
PI Luster AD, Leder P, Rothenberg M, Garcia E;
XX
DR WPI; 2002-565447/60.
XX
PT New DNA encoding murine, guinea pig or human eotaxin polypeptides,
PT useful for treating inflammation and tumorigenesis and in anticancer
PT gene therapy -
XX
PS Disclosure; Fig 3B; 42pp; English.
XX
CC The invention relates to polynucleotides encoding murine, guinea pig or
CC human eotaxin polypeptides. The eotaxin polynucleotides are useful for
CC modulating eosinophil chemotaxis, for increasing eosinophil chemotactic
CC events, and for improving prognosis with tumours in patients. They are
CC also useful for treating inflammation and tumourigenesis, and for
CC reducing inflammation and cytotoxic damage caused by eosinophils, for
CC e.g. during asthmatic reactions, eosinophilic pneumonia and allergic
CC diseases, inflammatory bowel diseases, atopic dermatitis, urticaria,
CC vasculitis, parasitic infections and eosinophil cardiac diseases. The
CC eotaxin polynucleotides are also useful for modulating histamine release
CC by modulating eotaxin activity or expression during anaphylaxis,
CC urticaria and allergic reactions. They are useful for detecting and
CC monitoring eosinophil mediating conditions, and in anti-cancer gene
CC therapy. The present sequence represents a human monocyte chemoattractive
CC protein (MCP)2 fragment.
XX
SQ Sequence 77 AA;

Query Match 72.7%; Score 412; DB 23; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.8e-41;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AQPDSVSIPITCCFNVINRKIPQRLSYTRITNIQCPKEAVIFKTRGKEVCADPKERW 92
Db 1 AQPDSVSIPITCCFNVINRKIPQRLSYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60
QY 93 VRDSMKHLDDIFQNLKP 109
Db 61 VRDSMKHLDDIFQNLKP 77

RESULT 11
AAO21099
ID AAY69031 standard; protein; 76 AA.
XX
AC AAY69031;
XX
DT 30-MAY-2000 (first entry)
XX
DE Amino acid sequence of chemokine receptor ligand MCP-2.
XX
KW Chemokine receptor; ligand; inflammatory response; immune effector cell;
KW secondary tissue damage; central nervous system injury; MCP-2;

KW CNS inflammatory disease; neurodegenerative disorder; heart disease;
KW inflammatory eye disease; inflammatory bowel disease;
KW inflammatory joint disease; inflammatory kidney; renal disease;
KW inflammatory lung disease; inflammatory nasal disease;
KW inflammatory thyroid disease; thyroiditis; cytokine-regulated cancer.
XX
OS Homo sapiens.
XX
PN WO200004926-A2.
XX
PD 03-FEB-2000.
XX
PF 21-JUL-1999; 99WO-CA00659.
XX
PR 22-JUL-1998; 98US-0120523.
XX
PA (OSPR-) OSPREY PHARM LTD.
XX
PI McDonald JR, Coggin PJ;
XX
DR WPI; 2000-182542/16.
XX
PT A new therapeutic agent comprising a conjugate for treating secondary
PT tissue damage and other disease conditions like Alzheimer's disease,
PT stroke, Parkinson's disease and atherosclerosis -
XX
PS Disclosure; Page 60; 204pp; English.
XX
CC The present sequence represents a chemokine receptor ligand. The present
CC ligand can be incorporated into the conjugates of the invention. The
CC specification describes a conjugate, comprising a targeted agent and a
CC chemokine receptor ligand. The conjugate binds to a chemokine receptor
CC resulting in internalisation of the targeted agent in cells bearing the
CC receptor. The conjugates are used for formulating a medicament or for
CC treating disorders associated with inflammatory responses resulting from
CC activation, proliferation and migration of immune effector cells. The
CC disorders or disease states comprise secondary tissue damage such as
CC central nervous system (CNS) injury, CNS inflammatory diseases,
CC neurodegenerative disorders, heart disease, inflammatory eye diseases,
CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory
CC kidney or renal diseases, inflammatory lung diseases, inflammatory
CC nasal diseases, inflammatory thyroid disease such as thyroiditis, or
CC cytokine-regulated cancers.
XX
SQ Sequence 76 AA;

Query Match 72.0%; Score 408; DB 21; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QPDSVSIPITCCFNVINRKIPQRLSYTRITNIQCPKEAVIFKTRGKEVCADPKERW 93
Db 1 QPDSVSIPITCCFNVINRKIPQRLSYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60
QY 94 RDSMKHLDDIFQNLKP 109
Db 61 RDSMKHLDDIFQNLKP 76

RESULT 12
AAO21099
ID AAO21099 standard; protein; 76 AA.
XX
AC AAO21099;
XX
DT 19-JUL-2002 (first entry)
XX
DE Protein of WT-MCP-2.
XX
KW RANTES; neuroprotective; antiallergic; antiinflammatory; anti-HIV; human;
KW chemokine mutant; cationic site; multiple sclerosis; HIV infection;
KW inflammatory disease; demyelinating disease; allergic.

OS Homo sapiens.
XX
PN WO200228419-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-EP11428.
XX
PR 04-OCT-2000; 2000EP-0121665.
XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX PI Proudfoot A, Wells TNC, Kosco-Vilbois M;
XX
DR WPI; 2002-340073/37.
XX
PT A mutant of the human CC chemokine RANTES with two mutations in the
PT cationic site of the 40's loop is used for treatment of multiple
PT sclerosis and/or demyelinating diseases -
XX
XX
PS Examples; Page 46; 46pp; English.
XX
CC The invention relates to a truncated and mutated human RANTES (a CC
CC chemokine mutant), comprising the amino sequence of 91 amino acids as
CC given in the specification. The CC chemokine mutant RANTES, with two
CC mutations in the cationic site is useful for the preparation of a
CC pharmaceutical composition used in treating multiple sclerosis or other
CC demyelinating diseases. The mutant with single mutations at cationic
CC sites is used for the treatment of HIV infection and/or other allergic or
CC inflammatory diseases. This sequence represents an example of a wild-type
CC chemokine protein used in the invention.
XX
SQ Sequence 76 AA;

Query Match 72.0%; Score 408; DB 23; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 QPDSVSIPITCCFNVINRKIPIQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERWV 93
Db 1 QPDSVSIPITCCFNVINRKIPIQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERWV 60

OY 94 RDSMKHLDQIFQNLKP 109
Db 61 RDSMKHLDQIFQNLKP 76

RESULT 13
AAO21109
ID AAO21109 standard; Protein; 76 AA.
XX
AC AAO21109;
XX
DT 19-JUL-2002 (first entry)
XX
DE MCP-2 chemokine protein containing 40's loop and cationic site.
XX
KW RANTES; neuroprotective; antiallergic; antiinflammatory; anti-HIV; human;
KW chemokine mutant; cationic site; multiple sclerosis; HIV infection;
KW inflammatory disease; demyelinating disease; allergic.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
FH Region 36..52
FT /label= 40's_loop
FT Misc-difference 46..49
FT /label= Cationic_site
XX
XX WO200228419-A2.
XX
XX 11-APR-2002.
XX

PF 03-OCT-2001; 2001WO-EP11428.
XX
XX
PR 04-OCT-2000; 2000EP-0121665.
XX
XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
XX PI Proudfoot A, Wells TNC, Kosco-Vilbois M;
XX
XX
DR WPI; 2002-340073/37.
XX
XX
PT A mutant of the human CC chemokine RANTES with two mutations in the
PT cationic site of the 40's loop is used for treatment of multiple
PT sclerosis and/or demyelinating diseases -
XX
XX
PS Disclosure; Fig 1; 46pp; English.
XX
XX
CC The invention relates to a truncated and mutated human RANTES (a CC
CC chemokine mutant), comprising the amino sequence of 91 amino acids as
CC given in the specification. The CC chemokine mutant RANTES, with two
CC mutations in the cationic site is useful for the preparation of a
CC pharmaceutical composition used in treating multiple sclerosis or other
CC demyelinating diseases. The mutant with single mutations at cationic
CC sites is used for the treatment of HIV infection and/or other allergic or
CC inflammatory diseases. This sequence represents an example of a CC
CC chemokine protein containing a 40's loop and cationic site of the
XX
XX
SQ Sequence 76 AA;

Query Match 72.0%; Score 408; DB 23; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 QPDSVSIPITCCFNVINRKIPIQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERWV 93
Db 1 QPDSVSIPITCCFNVINRKIPIQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERWV 60

OY 94 RDSMKHLDQIFQNLKP 109
Db 61 RDSMKHLDQIFQNLKP 76

RESULT 14
AAG78390
ID AAG78390 standard; protein; 76 AA.
XX
AC AAG78390;
XX
DT 30-MAY-2002 (first entry)
XX
DE Human chemokine hMCP-2.
XX
KW Antigen presenting cell; APC; chemotaxin; immune response; antigen;
KW chemokine; antitumour; cytostatic; antimicrobial; toxin;
KW pathogenic agent; cancer; melanoma; thyroid carcinoma;
KW renal cell carcinoma; tumour-associated antigen; human; hMCP-2.
XX
OS Homo sapiens.
XX

PF 20-APR-2001; 2001WO-US12950.
XX
XX
PR 21-APR-2000; 2000US-198839P.
PR 12-APR-2001; 2001US-0834814.
XX
XX
PA (CHEM-) CHEMOCENTRIX INC.
XX
XX Schall TJ, Talbot D;
XX
XX WPI; 2002-034405/04.
XX

XX Use of a composition containing an antigen presenting cell-chemotaxin
PT which is a chemokine polypeptide or its variant or a polynucleotide
PT encoding the protein, for inducing immune response to an antigen in a
PT subject
XX
PS
PS Claim 7; Fig 2; 60pp; English.
XX
XX The present sequence is that of a human chemokine polypeptide designated
CC hMCP-2, used in the compositions of the invention. The specification
CC describes the use of a composition containing an antigen presenting cell
CC (APC)-chemotaxin for inducing an immune response to an antigen in a
CC subject, in the manufacture of a medicament, where the APC-chemotaxin is
CC a chemokine polypeptide or its variant, or a polynucleotide encoding the
CC chemokine polypeptide or its variant. The invention has antitumour,
CC cytostatic and antimicrobial activity. The compositions of the invention
CC can contain one or more antigens (or antigen containing polynucleotides)
CC and may be administered in the same mixture as the APC-chemotaxin or
CC separately. Synthetic (mimetic) or naturally occurring chemokines may be
CC used. The polypeptides of the invention are used to induce an immune
CC response by recruiting APCs to areas of antigen contact. The compositions
CC of the invention are useful for providing protection from foreign
CC infectious pathogenic agents (bacteria, virus, etc.,) prior to expected
CC or possible exposure; for treating cancers, melanomas,
CC thyroid carcinomas, lung and breast cancers, renal cell carcinomas etc.,
CC here the antigen present in the composition is a tumour-associated
CC antigen. The use of APC-chemotaxins provides an accelerated immune
CC response in a host following administration of antigen, a more effective
CC response to administration of, or exposure to, very small quantities of
CC an antigen (e.g., toxin or pathogen) due to increased antigen uptake by
CC APCs, and more effective anti-tumour therapies.
XX
XX
XX Sequence 76 AA;

XX Schall TJ, Talbot D;
PI
XX
DR WPI; 2002-049246/06.
XX
PT Inducing an immune response to an antigen to confer non-specific
PT protection while the body is generating the adaptive response,
PT comprises administering a composition containing an antigen-presenting
PT cell chemotaxin -
XX
PS
PS Example 5; Fig 2; 60pp; English.
XX
XX The present invention describes a method for inducing an immune response
CC to an antigen in a subject. The method comprises administering a
CC composition containing an antigen-presenting cell chemotaxin
CC (APC-chemotaxin), where the APC-chemotaxin is a chemokine polypeptide,
CC its variant, or a polynucleotide encoding the chemokine polypeptide or
CC its variant. The APC-chemotaxin has cytostatic, antimicrobial and
CC immunostimulant activities, and can be used in vaccine production.
CC The method can be used for inducing or enhancing an immune response,
CC or for providing protection from exogenous foreign infectious pathogenic
CC agents prior to expected or possible exposure, or to individuals
CC displaying symptoms of exposure. The method may be used to treat cancers
CC e.g. breast cancer, lung cancer, carcinomas, melanomas, and tumours.
CC The present sequence represents a human monocyte chemotactic protein 2
CC (hMCP2) amino acid sequence, which is used in an example from the
CC present invention for the design of hybridines (chimeric chemokines).
SQ
XX Sequence 76 AA;

Query Match	71.3%;	Score 404;	DB 23;	Length 76;
Best Local Similarity	98.7%;	Pred. No. 3.3e-40;		
Matches 75; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

	Query Match	71.3%;	Score 404;	DB 23;	Length 76;
	Best Local Similarity	98.7%;	pred. No. 3.3e-40;		
	Matches	75;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0
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Db	1 QPDSVSIPTCCFNVINRKIPIDRIESTYTRITNIQCCKEAVIEFKTKRGKEVCADPKERWV	60			

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QY 34 QPDSVSIPTCCFNVINRKPIQRLSEYTRITNIQCPEAVIFRTKRGKEVCADPKERWV 93
  |||
Db 1 QPDSVSIPTCCFNVINRKPIQRLSEYTRITNIQCPEAVIFRTKRGKEVCADPKERWV 60
  |||
QY 94 RDSMKHLDOIQNLRP 109
  |||
Db 61 RDSMKHLDOIQNLRP 76
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Search completed: February 18, 2003, 03:02:52
Job time : :71 secs

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      Job time : :71 secs

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RESULT	15
AAG68353	
ID	AAG68353 standard; peptide; 76 AA.
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AC	AAG68353;
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DT	01-MAR-2002 (first entry)
XX	
DE	Human monocyte chemotactic protein 2 (MCP2) amino acid sequence.
XX	
KW	Human; mouse; monocyte chemotactic protein 2; hMCP2; MCP2; mC10; mMDC;
KW	chimeric chemokine; immune response; cytostatic; antimicrobial;
KW	immunostimulant; vaccine; cancer; breast cancer; lung cancer;
KW	carcinoma; melanoma; tumour; hybridoma.
XX	
OS	Homo sapiens.
XX	
PN	W0200180887-A2.
XX	
PD	01-NOV-2001.
XX	
PF	12-APR-2001; 2001WO-US12162.
XX	
PR	21-APR-2000; 2000US-198839P.
XX	
PA	(CHEM-) CHEMOCENTRIX INC.

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2003, 03:03:01 ; Search time 19 Seconds

(without alignments)
146.570 Million cell updates/sec

Title: US-10-033-067-1

Perfect score: 567
Sequence: 1 MLKLTPLPSKMKVSAALLCL.....ERWVRDSMKHLDQIFQNLKP 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA: *
1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567	100.0	109	9	US-10-033-067-1 Sequence 1, Appli
2	412	72.7	77	8	US-08-927-939-17 Sequence 17, Appl
3	412	72.7	77	9	US-10-057-275-10 Sequence 10, Appl
4	412	72.7	77	9	US-09-834-794A-24 Sequence 24, Appl
5	412	72.7	77	10	US-09-834-795A-24 Sequence 24, Appl
6	408	72.0	76	9	US-09-792-793A-21 Sequence 21, Appl
7	396	69.8	74	10	US-09-195-457-6 Sequence 6, Appli
8	375	66.1	97	9	US-10-057-275-5 Sequence 5, Appli
9	367	64.7	99	8	US-08-927-939-16 Sequence 16, Appl
10	367	64.7	99	9	US-10-057-275-9 Sequence 9, Appli
11	367	64.7	99	9	US-10-033-067-4 Sequence 4, Appli
12	367	64.7	99	9	US-10-141-965-5 Sequence 5, Appli
13	357	63.0	109	9	US-10-057-275-11 Sequence 11, Appl
14	357	63.0	109	9	US-10-033-067-3 Sequence 3, Appli
15	354	62.4	99	9	US-09-834-794A-28 Sequence 28, Appl
16	354	62.4	99	10	US-09-834-795A-28 Sequence 28, Appl
17	350	61.7	97	8	US-08-927-939-25 Sequence 25, Appl
18	350	61.7	97	9	US-10-114-893-52 Sequence 52, Appl
19	350	61.7	97	9	US-09-834-794A-26 Sequence 26, Appl

20	350	61.7	97	10	US-09-834-795A-26	Sequence 26, Appl
21	346	61.0	97	9	US-10-057-275-2	Sequence 2, Appli
22	337	59.4	99	8	US-08-927-939-18	Sequence 18, Appl
23	337	59.4	99	9	US-10-125-451-18	Sequence 18, Appl
24	332	58.6	99	9	US-09-834-794A-27	Sequence 27, Appl
25	332	58.6	99	10	US-09-834-795A-27	Sequence 27, Appl
26	328.5	57.9	98	8	US-08-927-939-50	Sequence 50, Appl
27	328.5	57.9	98	8	US-08-927-939-83	Sequence 83, Appl
28	328.5	57.9	98	9	US-10-164-621-4	Sequence 4, Appli
29	328.5	57.9	98	9	US-10-125-451-4	Sequence 4, Appli
30	328.5	57.9	98	9	US-09-834-794A-25	Sequence 25, Appl
31	328.5	57.9	98	10	US-09-834-795A-25	Sequence 25, Appl
32	328.5	57.9	98	10	US-09-872-611A-2	Sequence 2, Appli
33	268	47.3	76	9	US-09-792-793A-20	Sequence 20, Appl
34	268	47.3	76	10	US-09-195-457-5	Sequence 5, Appli
35	268	47.3	325	9	US-09-792-793A-71	Sequence 71, Appl
36	268	47.3	327	9	US-09-792-793A-72	Sequence 72, Appl
37	268	47.3	332	9	US-09-792-793A-73	Sequence 73, Appl
38	267	47.1	74	9	US-09-792-793A-13	Sequence 13, Appl
39	267	47.1	74	9	US-10-125-451-20	Sequence 20, Appl
40	267	47.1	323	9	US-09-792-793A-80	Sequence 80, Appl
41	267	47.1	325	9	US-09-792-793A-81	Sequence 81, Appl
42	267	47.1	330	9	US-09-792-793A-82	Sequence 82, Appl
43	259	45.7	148	8	US-08-927-939-26	Sequence 26, Appl
44	243	42.9	76	9	US-09-792-793A-22	Sequence 22, Appl
45	243	42.9	76	9	US-10-125-451-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-033-067-1
; Sequence 1, Application US/10033067
; Patent No. US20020164704A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROTEIN
; FILE REFERENCE: PF-0069-1 CON
; CURRENT APPLICATION NUMBER: US/10/033, 067
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 08/683, 655
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020164704A1 965517CD1
US-10-033-067-1
Query Match 100.0%; Score 567; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.6e-53;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MLKLTPLPSKMKVSAALLCLLMAATFSPQGLAQPDVSSTPTCCFNVINRKIPQRLS 60
Db 1 MLKLTPLPSKMKVSAALLCLLMAATFSPQGLAQPDVSSTPTCCFNVINRKIPQRLS 60
OY 61 YTRITNIQCPKEAVIFKTRKGEVCADPKERWVRDSMKHLDQIFQNLKP 109
Db 61 YTRITNIQCPKEAVIFKTRKGEVCADPKERWVRDSMKHLDQIFQNLKP 109
RESULT 2
US-08-927-939-17
; Sequence 17, Application US/08927939
; Patent No. US20010006640A1


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; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-927-939-17

Query Match          72.7%; Score 412; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.3e-37;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AOPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKEVCADPKERW 92
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Db 1 AOPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKEVCADPKERW 60
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QY 93 VRDSMKHLDQIFQNLKP 109
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Db 61 VRDSMKHLDQIFQNLKP 77

RESULT 3
US-10-057-275-10
; Sequence 10, Application US/10057275
; Patent No. US2002015545A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; Bandman, Olga
; Wilde, Craig G.
; TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/057,275
; FILING DATE: 25-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,740A
; FILING DATE: February 17, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0027 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
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; CLONE: MCP-2
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-057-275-10

Query Match          72.7%; Score 412; DB 9; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.3e-37;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AOPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKEVCADPKERW 92
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Db 1 AOPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKEVCADPKERW 60
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QY 93 VRDSMKHLDQIFQNLKP 109
      |||
Db 61 VRDSMKHLDQIFQNLKP 77

RESULT 4
US-09-834-794A-24
; Sequence 24, Application US/09834794A
; Publication No. US20030026777A1
; GENERAL INFORMATION:
; APPLICANT: Lawrence, Papsidero
; APPLICANT: Lyn, Dyster
; APPLICANT: Jana, Frustaci
; TITLE OF INVENTION: Detection and Treatment of Breast Cancer
; FILE REFERENCE: 3380/11127-US4
; CURRENT APPLICATION NUMBER: US/09/834,794A
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/146,580
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/071,899
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 60/092,155
; PRIOR FILING DATE: 1998-07-09
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-794A-24

Query Match          72.7%; Score 412; DB 9; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.3e-37;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AOPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKEVCADPKERW 92
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Db 1 AOPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKEVCADPKERW 60
      |||

QY 93 VRDSMKHLDQIFQNLKP 109
      |||
Db 61 VRDSMKHLDQIFQNLKP 77

RESULT 5
US-09-834-795A-24
; Sequence 24, Application US/09834795A
; Patent No. US20020076710A1
; GENERAL INFORMATION:
; APPLICANT: Lawrence, Papsidero
; APPLICANT: Lyn, Dyster
; APPLICANT: Jana, Frustaci
; TITLE OF INVENTION: Detection and Treatment of Breast Cancer
; FILE REFERENCE: 3380/11127-US3
; CURRENT APPLICATION NUMBER: US/09/834,795A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 09/146,580
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/071,899
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 60/092,155
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;; PRIOR FILING DATE: 1998-07-09
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: Patentln version 3.0
;; SEQ ID NO 24
;; LENGTH: 77
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-834-795A-24

Query Match 72.7%; Score 412; DB 10; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.3e-37;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AQPDSVIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 92
Db 1 AQPDSVIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60

QY 93 VRDSMKHLDQIFQNLKP 109
Db 61 VRDSMKHLDQIFQNLKP 77

RESULT 6
US-09-792-793A-21

;; Sequence 21, Application US/09792793A
;; Patent No. US20020168370A1
;; GENERAL INFORMATION:
;; APPLICANT: McDonald, John R.
;; APPLICANT: Coggin, Philip
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;; FILE REFERENCE: 25020-601D
;; CURRENT APPLICATION NUMBER: US/09/792,793A
;; CURRENT FILING DATE: 2001-02-22
;; NUMBER OF SEQ ID NOS: 93
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 21
;; LENGTH: 76
;; TYPE: PRT
;; ORGANISM: homo sapien
;; FEATURE:
;; OTHER INFORMATION: Human Chemokine Polypeptide: MCP-2
US-09-792-793A-21

Query Match 72.0%; Score 408; DB 9; Length 76;
Best Local Similarity 100.0%; Pred. No. 8.6e-37;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QPDSVIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 93
Db 1 QPDSVIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60

QY 94 RDSMKHLDQIFQNLKP 109
Db 61 RDSMKHLDQIFQNLKP 76

RESULT 7
US-09-195-457-6

;; Sequence 6, Application US/09195457
;; Patent No. US20020081623A1
;; GENERAL INFORMATION:
;; APPLICANT: WILLIAMS, TIMOTHY J.
;; APPLICANT: JOSE, PETER J.
;; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
;; APPLICANT: HSUAN, JOHN J.
;; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
;; FILE REFERENCE: 550-33
;; CURRENT APPLICATION NUMBER: US/09/195,457
;; CURRENT FILING DATE: 1998-11-18
;; PRIOR APPLICATION NUMBER: 08/470,323
;; PRIOR FILING DATE: 1995-06-06
;; PRIOR APPLICATION NUMBER: PCT/GB94/02006

;; PRIOR FILING DATE: 1994-09-14
;; PRIOR APPLICATION NUMBER: GB 9318984.3
;; PRIOR FILING DATE: 1993-09-14
;; PRIOR APPLICATION NUMBER: GB 94086902.2
;; PRIOR FILING DATE: 1994-04-29
;; NUMBER OF SEQ ID NOS: 11
;; SEQ ID NO 6
;; LENGTH: 74
;; TYPE: PRT
;; ORGANISM: human
US-09-195-457-6

Query Match 69.8%; Score 396; DB 10; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.6e-35;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 DSVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 95
Db 1 DSVSIPITCCFNVINRKIPQRLSEYTRITNIQCPKEAVIFKTRGKEVCADPKERW 60

QY 96 SMKHLDDQIFQNLKP 109
Db 61 SMKHLDDQIFQNLKP 74

RESULT 8
US-10-057-275-5

;; Sequence 5, Application US/10057275
;; Patent No. US2002015545A1
;; GENERAL INFORMATION:
;; APPLICANT: Coleman, Roger
;; APPLICANT: Bandman, Olga
;; APPLICANT: Wilde, Craig G.
;; TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: U.S.
;; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/057,275
;; FILING DATE: 25-Jan-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/390,740A
;; FILING DATE: February 17, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Luther, Barbara J.
;; REGISTRATION NUMBER: 33,954
;; REFERENCE/DOCKET NUMBER: PF-0027 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-852-0195

;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 97 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-057-275-5

Query Match 66.1%; Score 375; DB 9; Length 97;
Best Local Similarity 74.7%; Pred. No. 3.7e-33;
Matches 74; Conservative 7; Mismatches 16; Indels 2; Gaps 1;

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QY      11 MKVSALLCLLMAATSFQGLAQDPDSVIPITCCFNVINRKIPQRLSEYTRITNIOCP 70
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Db      1 MKVSALLALLIAAFCDQGLAQDPDGVDPPTCCFNVINRKIPQRLSEYRITSSKCS 60
QY      71 KEAVIFKTKRGKEVCADPEKRWVRDSMKHLDOIQNLP 109
        | ||||| | :||| | :||| | :| |
Db      61 KPAVIFKTKRAKQVCADPEKRWQDSMKHLDK--QTPKP 97

RESULT 9
US-08-927-939-16
; Sequence 16, Application US/08927939
; Patent No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Laven Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-927-939-16

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Query Match          64.7%; Score 367; DB 8; Length 99;
Best Local Similarity 69.4%; Pred. No. 2.7e-32;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

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DB 1 MKVSALLCLLLIAATFIPQGLAQPDAINAPVTCYNTFRKRISYQRLASYSRRTSSKCP 60

QY 71 KEAVIFKTRGKEVCADPKERNVNRDSMKHLDOIQNLK 108
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DB 61 KEAVIFKTIVAKEICADPKQKQWQDSMDHLDKOTQTPK 98

RESULT 10
US-10-057-275-9
; Sequence 9, Application US/10057275
; Patent No. US20020155545A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; Bandman, Olga
; Wilde, Craig G.
; TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/057,275
; FILING DATE: 25-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,740A
; FILING DATE: February 17, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.

```

```

;
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0027 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 99 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
;   LIBRARY: GenBank
;   CLONE: MCP-1
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-057-275-9

Query Match          64.7%; Score 367; DB 9; Length 99;
Best Local Similarity 69.4%; Pred. No. 2.7e-32;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 11 MKVSALLCLLMAATFSPQGLAQPDSVISIPITCCENVYNRKIPRIQRLSEYTRITNIQCP 70
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MKVSALLCLLLIAATFIPQGLAQPDAINAPVTCCTNFTNRKISVQLASRYRITSSKCP 60

QY 71 KEAVIFKTKRGKEVCADPKERKRWVSDSMKHLDDQIFQNLK 108
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 KEAVIFKTIYAKETICADPKRQKRWQDSMDHLDDKQGTQTPK 98

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RESULT 11
US-10-033-067-4
; Sequence 4, Application US/10033067
; Patent No. US20020164704A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROTEIN
; FILE REFERENCE: PF-0069-1 CON
; CURRENT APPLICATION NUMBER: US/10/033,067
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 08/683,655
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20020164704A1 g338809
US-10-033-067-4

Query Match          64.7%; Score 367; DB 9; Length 99;
Best Local Similarity 69.4%; Pred. No. 2.7e-32;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0.

QY 11 MKVSALLCLLMAATFSPQGLAQPDSVIPITCCFNVINRKIPIORLESYTRITNIQCP 70
      |||||  |||||  |||||  |||||  ::  |::|  |  |||  ||  |||  ::||
DB 1  MKVSALLCLLIAATFIPOGLAQDAINAPVTCYNTFTNRKISVORLASYRRTSSKCP 60

QY 71 KEAVIFKTKRGKEVCADPKERWVRDMSMKHLDOIFONLK 108
      |||||  ||  |||||  ::|||  |||  |||  |
DB 61 KEAVIFKTIVAKEICADPKQKRWQDSMDHLDKQTQTPK 98

RESULT 12
US-10-141-965-5
; Sequence 5, Application US/10141965
; Publication No. US20020182200A1

```

```

; GENERAL INFORMATION:
; APPLICANT: LI, HAODONG
; RUBEN, STEVEN M
; SUTTON, GRANGER G III
; TITLE OF INVENTION: HUMAN CHEMOTACTIC PROTEIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/141,965
; FILING DATE: 10-May-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/453,416
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: US 09/044,855
; FILING DATE: 20-MAR-1998
; APPLICATION NUMBER: US 08/479,126
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/424,425
; FILING DATE: 21-APR-1995
; APPLICATION NUMBER: PCT/US94/05384
; FILING DATE: 16-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: STEEFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.034000C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-141-965-5

Query Match          64.7%; Score 367; DB 9; Length 99;
Best Local Similarity 69.4%; Pred.No. 2.7e-32;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;;

QY      11 MKVSAALLCLLMAATFSOGLAOPDSVSIPITCCFNVINRKIPIORLESYTRITNIOCP 70
        |||||||:|||||||:|||||:|:|||||:|||||||:|||||:|||||:|||||:
Db       1 MKVSAALLCLLLIAATFIPOGLAQPDAINAVPTCCYNFTNRKISVQRLASYSRTSSKCP 60
QY      71 KEAVIFKTKRGKEVCADPKRWVRSDSMKHLDOI FQNLR 108
        ||||||| |:|||||::||:|||| | | | |
Db      61 KEAVIFKTIYAKEICADPRQKWVDSDMDHLDKQTQTPK 98

RESULT 13
; Sequence 11, Application US//10057275
; Patent No. US20020155545A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; Bandman, Olga
; Wilde, Craig G.
; TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

```

```

ADDRESSSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/057,275
FILING DATE: 25-Jan-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/390,740A
FILING DATE: February 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0027 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: MCP-3

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-057-275-11

Query Match 63.0%; Score 357; DB 9; length 109;
Best Local Similarity 63.9%; Pred. No. 3.5e-31;
Matches 69; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 1 MLKLTPLPSKMKVSAALICLLMAATFSPQGLAQPDSVSIPTTCGFNVINKPIORLES 60
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MWKPMSPSPSNMKASALICLLLTAAAFSPQGLAQPVGINTSTTCYRINKKIPKORLES 60
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 YTRITNIQCPKEAVIFKTRKGKEVCADPKERWVRDSMKHLDQIFQNLK 108
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 YRRITSSHCPREAVIFKTKLDKEICADPTQKWVQDFMKHLDKKTQTPTK 108

RESULT 14
US-10-033-067-3
; Sequence 3, Application US/10033067
; Patent No. US20020164704A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROTEIN
; FILE REFERENCE: PF-0069-1 CON
; CURRENT APPLICATION NUMBER: US/10/033,067
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 08/683,655
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 18, 2003, 03:00:21 ; Search time 40 Seconds
(without alignments)
261.966 Million cell updates/sec

Title: US-10-033-067-1
Perfect score: 567
Sequence: 1 MLKLTPLPSKMKVSAALLCL.....ERWVRDSMKHLDOI FQNLKP 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB	ID	Description
1	513	90.5	99	2	JC5295	monocyte chemotact
2	372	65.6	99	2	JC2417	monocyte chemotatr
3	367	64.7	99	2	A60299	monocyte chemotatr
4	357	63.0	109	2	A54678	monocyte chemotact
5	349	61.6	97	2	JC4912	eotaxin precursor
6	339	59.8	99	2	JC2136	monocyte chemotatr
7	302	53.3	99	1	A39296	monocyte chemotatr
8	302	53.3	99	2	JC2336	monocyte chemotatr
9	298	52.6	125	2	I46857	eotaxin precursor
10	280.5	49.5	96	2	I48099	eotaxin precursor
11	273.5	48.2	96	2	JC2478	eotaxin precursor
12	259	45.7	148	1	A30209	PDGF-inducible JE
13	255	45.0	120	2	I48147	monocyte chemotatr
14	250	44.1	148	1	S07723	immediate-early se
15	244	43.0	97	2	A48093	monocytic cytokine
16	219	38.6	72	2	A55984	monocyte chemotact
17	183.5	32.4	93	2	B35673	LD78-beta protein
18	174.5	30.8	92	1	A31767	macrophage inflamm
19	169.5	29.9	92	2	C30552	macrophage inflamm
20	169.5	29.9	92	2	I46730	immune activation
21	163	28.7	92	2	A32393	macrophage inflamm
22	159	28.0	92	2	A30574	macrophage inflamm
23	158	27.9	92	2	I52322	macrophage inflamm
24	157	27.7	91	1	A28815	monocyte chemotatr
25	149	26.3	91	1	A46539	monocyte chemotatr
26	148.5	26.2	120	2	JE0177	lymphocyte and mon
27	136.5	24.1	96	2	A37236	I-309 protein - mou
28	135.5	23.9	92	2	S24236	ICAM3 protein - mou
29	127.5	22.5	114	1	ETHUL	lymphotactin precu

30	118.5	20.9	114	1	ETMSL	lymphotactin precu
31	104	18.3	50	2	C60407	monocyte adherence
32	97.5	17.2	116	2	I49555	gene C10 protein -
33	97	17.1	103	2	A53096	interleukin-8 prec
34	93	16.4	101	2	S42496	interleukin-8 prec
35	92	16.2	100	2	S46198	cytokine-induced n
36	90	15.9	117	2	B44253	alveolar macrophag
37	87	15.3	99	2	A37034	interleukin-8 prec
38	83.5	14.7	85	1	B30552	T-cell activation
39	83.5	14.7	98	1	TGHUGI	interferon gamma-i
40	83	14.6	95	2	JN0841	interleukin-8 - do
41	82	14.5	101	2	I48148	Neutrophil attract
42	81	14.3	132	2	A57325	C-X-C chemokine LI
43	80	14.1	101	2	I46871	interleukin-8 - ra
44	78	13.8	114	2	A55010	neutrophil-activat
45	75.5	13.3	100	2	JH0200	macrophage inflamm

ALIGNMENTS

RESULT 1
JC5295
monocyte chemotactic protein-2 precursor - human
C:Species: Homo sapiens (man)
C>Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C:Accession: JC5295
R:Van Collie, E.; Froyen, G.; Nomiya, H.; Miura, R.; Fiten, P.; Van Aelst, I.; Ve
Biochem. Biophys. Res. Commun. 231, 726-730, 1997
A:Title: Human monocyte chemotactic protein-2: cDNA cloning and regulated expression
A:Reference number: JC5295; MUID:97224420; PMID:9070881
A:Accession: JC5295
A:Molecule type: mRNA
A:Residues: 1-99 <VAN>
A:Cross-references: GB:Y10802; NID:g1924937; PIDN:CAA71760.1; PID:g1924938
A:Experimental source: bone marrow
C:Comment: This protein belongs to the beta-chemokine family which is one of the maj
tis and in tumor biology, and contribute to the trafficking and recruitment of the re
C:Genetics:
A:Gene: mcp-2
C:Superfamily: macrophage inflammatory protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-99/Product: monocyte chemotactic protein-2 #status predicted <MAT>

Query Match 90.5%; Score 513; DB 2; Length 99;
Best Local Similarity 99.08; Pred. No. 4.4e-49;
Matches 98; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 MKVSAALICLLMAATFSPQGLAQPDSVSIPTCCFNVINRKIPIORLESYTRITNIQCP 70
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Db 1 MKVSAALICLLMAATFSPQGLAQPDSVSIPTCCFNVINRKIPIORLESYTRITNIQCP 60

QY 71 KEAVIFKTKRKEVCADPKERWVRDSMKHLDOI FQNLKP 109
|||||
Db 61 KEAVIFKTKRKEVCADPKERWVRDSMKHLDOI FQNLKP 99

RESULT 2
JC2417
monocyte chemoattractant protein-2 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 16-Jul-1999
C:Accession: JC2417
R:Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wutke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 205, 148-153, 1994
A:Title: Porcine luteal cells express monocyte chemoattractant protein-2 (MCP-2): Ar
A:Reference number: JC2417; MUID:95091716; PMID:7999015
A:Accession: JC2417
A:Molecule type: mRNA
A:Residues: 1-99 <HOS>
A:Cross-references: GB:Z48480; NID:g683718; PIDN:CAA88371.1; PID:g683719
A:Experimental source: corpus luteum
C:Superfamily: macrophage inflammatory protein

A;Residues: 1-109 <OPD>
A;Cross-references: GB:X72309
R;Opdenacker, G.; Froyen, G.; Filten, P.; Proost, P.; Van Damme, J.
Biochem. Biophys. Res. Commun. 191, 535-542, 1993
A;Title: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA and
A;Reference number: JCl478; MUID:93213290; PMID:8461011
A;Accession: JCl478
A;Molecule type: mRNA
A;Residues: 1-109 <OP2>
A;Cross-references: GB:X72308; GB:S57464; NID:g3928270; PIDN:CA451055.1; PID:g313708
R;Minty, A.; Chalon, P.; Guillemot, J.C.; Kagnad, M.; Liauzun, P.; Magazin, M.; Miloux,
submitted to the EMBL Data Library, March 1993
A;Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoattractant
A;Reference number: S32222
A;Accession: S32222
A;Molecule type: mRNA
A;Residues: 1-109 <MIN>
A;Cross-references: EMBL:X71087; NID:g288396; PIDN:CA450405.1; PID:g288397
C;Comment: This protein induces proteinase secretion and chemotaxis by macrophages and m
C;Genetics:
A;Gene: GDB:SCYA7; SCYA6; MCP-3
A;Cross-references: GDB:138473; OMIM:158106
A;Map position: 17q11-17q12
A;Introns: 36/1; 75/2
C;Superfamily: macrophage inflammatory protein
C;Keywords: cytokine; glycoprotein; inflammation
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-109/Product: monocyte chemotactic protein 3 #status predicted <MAT>
F;39/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	63.0%;	Score 357;	DB 2;	Length 109;
Best Local Similarity	63.9%;	Pred. No. 6.5e-32;		
Matches 69;	Conservative 11;	Mismatches 28;	Indels 0;	Gaps 0;

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QY      1 MLKLTPLPSKMKVSAALLCULLMAATFSPQGLAQDSDVSIPTCCFNVINKRPIQRLES 60
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Db      1 MKKPMPSNNMKASALLCILLTAAAFSPQGLAPGINTSTCCYRINKKIPKORLES 600
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QY 61 YRTRITNIQCPEAVIFKTKRGKEVCADPKERWVRDSMKHLDQLFQNLK 108
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Db 61 YRRTTSSHCPRFAVIFKTKDKEICADPTOKWODFMKHLPKCTOTPK 108

RESULT 5
JC4912

eotaxin precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Jun-2000
 C/Accession: J04912
 R/Bartels, J.; Schlueter, C.; Richter, E.; Noso, N.; Kulke, R.; Christophers, E.; Schroe-
 Biochem. Biophys. Res. Commun. 225, 1045-1051, 1996
 A/Title: Human dermal fibroblasts express eotaxin: Molecular cloning, mRNA expression, a
 A/Reference number: J04912; MUID:96374440; PMID:8780731
 A/Accession: J04912
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-97 <BAR>
 A/Cross-references: EMBL:275668; NID:g1531982; PIDN:CAA99997.1; PID:g1531983
 A/Experimental source: dermal fibroblast
 C/Comment: This protein has eosinophil specific chemotactic activity.
 C/Superfamily: macrophage inflammatory protein
 C/Keywords: fibroblast
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-97/Product: eotaxin #status predicted <MAT>

Query Match	61.68;	Score 349;	DB 2;	Length 97;
Best Local Similarity	68.78;	Pred. No. 4.4e-31;		
Matches 68;	Conservative 13;	Mismatches 16;	Indels 2;	Gaps 1;

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QY      11 MKVSALLCLLMAATFSPQGLAQDPDSVIPITCCFNVINRKIPQLRLESYTRITNIQP 70
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Db      1 MKVSALLMLLLIAAFSPQGLTP--ASVPTTCFMANRKIPQLRLESYTRITSGKCP 58
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QY      71 KEAVIFKTKRGKEVCADPKERWVDSMKHLDFQNLKP 109
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Db      59 QKAVIEFKTKLAKDICADPKKRWQDSMKLYDQKSPTPRP 97
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RESULT
JC2136

monocyte chemoattractant protein-1 precursor - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 16-Jul-1999
C/Accession: J02136; S57498
R/Hosang, K.; Knoke, I.; Kraudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 199, 962-968, 1994
A/Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): An
A/Reference number: J02136; MUID:94183284; PMID:7510962
A/Accession: J02136
A/Molecule type: mRNA
A/Residues: 1-99 <HOS>
A/Cross-references: GB:Z48479; NID:g683716; PIDN:CAA88370.1; PID:g683717
R/Zach, O.
submitted to the EMBL Data Library, July 1994
A/Reference number: S57497
A/Accession: S57498
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-99 <ZAC>
A/Cross-references: EMBL:X79416; NID:g872312; PIDN:CAA55945.1; PID:g872313
C/Superfamily: macrophage inflammatory protein
C/Keywords: glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>
F:94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	59.8%;	Score 339;	DB 2;	Length 99;	.
Best Local Similarity	62.6%;	Pred. No. 5.6e-30;			.
Matches 62;	Conservative 19;	Mismatches 18;	Indels 0;	Gaps 0;	

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QY      ii MKVSALLCLLLMAATFSPQGLAQPDSVIPITCCENVINRKIPIQRLSESYTRLTNIQCP 70  
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Db      1 MKVSALLCLLTLTAATCTOVLAAOPDAINSPTVTCYTILTSKISMORLMYSRYRTSSKCP 60
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QY      71 KEAVIFKTRRGECADPKERWRDMSMKHLDDIFQNLP 109  
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Db     61 KEAVIFKTIGREICAEPRKOKWODSISLDDKNOTPKP 99
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RESULT 7
A39296

monocyte chemoattractant protein 1 precursor - bovine
N;Alternate names: monocyte chemotactic factor 1; seminal plasma protein P6
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A39296; B39296
R;Wempe, F.; Henschen, A.; Scheit, K.H.
DNA Cell Biol. 10, 671-679, 1991
A;Title: Gene expression and cDNA cloning identified a major basic protein constituent
A;Reference number: A39296; MUID:92096117; PMID:1721821
A;Accession: A39296
A;Molecule type: mRNA
A;Residues: 1-99 <WEM>
A;Cross-references: GB:M84602; GB:M85264; NID:g163394; PIDN:AAA30651.1; PID:g163395
A;Accession: B39296
A;Molecule type: protein
A;Residues: 50-68,'X','70-74','X','76 <WE2>
A;Experimental source: seminal vesicle
C;Superfamily: macrophage inflammatory protein
C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemoattractant protein 1 #status predicted <MAT>
F;94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	53.3%;	Score 302;	DB 1;	Length 99;
Best Local Similarity	56.68;	Pred. No. 6.5e-26;		


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A/Accession: A30209
A/Molecule type: DNA
A/Residues: 1-148 <ROL>
A/Cross-references: GB:M19681; NID:g193486; PIDN:AAA37684.1; PID:g387168; GB:M19682
J.Kawahara, R.S.; Deuel, T.F.
J. Biol. Chem. 264, 679-682, 1989
A>Title: Platelet-derived growth factor-inducible gene JE is a member of a family of sma
A/Reference number: A44771; MUID:89093129; PMID:2910858
A/Accession: A44771
A/Molecule type: DNA; mRNA
A/Residues: 1-148 <KA2>
A/Cross-references: GB:J04467; NID:g193488; PIDN:AAA37685.1; PID:g387169
C/Genetics:
A/Gene: JE
A/Introns: 26/1; 65/2
C/Superfamily: macrophage inflammatory protein
C/Keywords: cytokine; glycoprotein
F:126/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          45.7%; Score 259; DB 1; Length 148;
Best Local Similarity 53.3%; Pred. NO. 5.2e-21;
Matches 49; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

QY 11 MKVSALLCLLLMAATFSPQGLAOPDSVSIPTCCFNVINRKIPIQRLSEYTRITNIQCP 70
   1-1 11 11 1 11 111111: 1:1111: : 11: 1111 111: :11
DB 1 MQVPVMLLGLLFTVAGWSIHVLAQPDVAVNAPLTCYSFTSKMIPMSRLESYKRITSSRCP 60
   11111111 11 11111111 11: :1:11:

QY 71 KEAVIFKTKRGKEVCADPKERWVRDSMKHLDQ 102
   11111111 11 11111111 11: :1:11:
DB 61 KEAVVFVTKLKREVCADPKKEWVQTYIKNLDR 92

```

```

RESULT 13
148147
monocyte chemoattractant protein-1 - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C/Accession: I48147
R:Xoshimura, T.
J. Immunol. 150, 5025-5032, 1993
A>Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression of
A/Reference number: I48147; MUID:93267104; PMID:8496603
A/Accession: I48147
A>Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A:Residues: 1-120 <RES>
A/Cross-references: GB:I04985; NID:g349820; PIDN:AAA37047.1; PID:g349821
C:Genetics:
A:Gene: MCP-1
C/Superfamily: macrophage inflammatory protein

Query Match          45.0%; Score 255; DB 2; Length 120;
Best Local Similarity 52.2%; Pred. No. 1.1e-20;
Matches 48; Conservative 22; Mismatches 20; Indels 2; Gaps 2;

QY      11 MKVSALLCLLLMAATFSPQLAQPDVSIPTCCFNVINRKIPIQRLSESYRTINIQCP 70
       1 :| :|||||: |||| :||| | :| ||| : |:| | :| |
Db      1 MQRSSVLCLLVIEATFCSLMAQPGVNTP-TCCY-TFNKQIPLKRVKGERTSSRCP 58
               :||| | :| | | | | :||| :| |

QY      71 KEAVIFTKRGKEVCADPKERWVRDSMKHLDD 102
       :||| | :| | | | | :||| :| |
Db      59 QEAVIFRTLKNKEVCADPTOKWVDYIAKLDD 90
               :||| | :| | | | | :||| :| |

RESULT 14
S07723
Immediate-early serum-responsive protein JE precursor - rat
N/Alternate names: monocyte chemoattractant protein-1
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: S07723; JN0128
R/Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.
Nucleic Acids Res. 18, 23-34, 1990

```

A;Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essen
A;Reference number: S07723; MUID:90174947; PMID:2106664
A;Accession: S07723
A;Molecule type: DNA
A;Residues: 1-148 <TIM>
A;Cross-references: EMBL:X17053; NID:g55530; PIDN:CAA34901.1; PID:g55531
R;Yoshimura, T.; Takeya, M.; Takahashi, K.
Biochem. Biophys. Res. Commun. 174, 504-509, 1991
A;Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its
A;Reference number: JN0128; MUID:91128376; PMID:1704226
A;Accession: JN0128
A;Molecule type: mRNA
A;Residues: 1-148 <YOS>
A;Cross-references: GB:M57441; NID:g205333; PIDN:AAA63496.1; PID:g205334
A;Experimental source: spleen cells
A;Note: the authors translated the codon GAA for residue 62 as Lys and GCT for resi
C;Genetics:
A;Introns: 26/1; 65/2
C;Superfamily: macrophage inflammatory protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-148/Product: immediate-early serum-responsive protein JE #status predicted <MA

Query Match	44.1%;	Score 250;	DB 1;	Length 148;
Best Local Similarity	50.0%;	Pred. No. 5e-20;		
Matches 46;	Conservative 19;	Mismatches 27;	Indels 0;	Gaps 0;

QY 11 MKVSALLCLLLMAATFSQGLAOPDSVIPITCCFNVINRKPIQRLSEYTRITNIQCP 70
1:11 11 11 1 1 1:111:1 1:111:1 : 11:111:1 11: 11
Db 1 MQVSVTLGLLFTVAACSIHVLSQLPDVAVNAPLTCCTCYSTFGKMIIPMSRLENYKRITSSRCP 60
11:111:1 11 1:1111: 11: : 111
QY 71 KEAVIFKTKRGKEVCADPKERKRWVRDSMKHLDO 102
1111:1 11 1:1111: 11: : 111
Db 61 KEAVVEVTKLKREICADPNKEWVQKIRKLDQ 92

RESULT 15
A48093
monocytic cytokine FIC - mouse
N/Alternate names: intercrine/chemokine; MARC/FIC protein; monocyte chemotactic pro
C/Species: Mus musculus (house mouse)
C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C/Accession: A48093; JC2452; S30592; I49630
R/Heinrich, J.N.; Ryseck, R.P.; Macdonald-Bravo, H.; Bravo, R.
Mol. Cell. Biol. 13, 2020-2030, 1993
A/Title: The product of a novel growth factor-activated gene, fic, is a biologically
A/Reference number: A48093; MUID:93204948; PMID:8455595
A/Accession: A48093
A/Molecule type: mRNA
A/Residues: 1-97 <HEI>
A/Cross-references: GB:L04694; NID:g192925; PIDN:AAA37516.1; PID:g192926
A/Experimental source: NIH 3T3 cells
R/Thirion, S.; Nys, G.; Fliten, P.; Masure, S.; Damme, J.V.; Opdenakker, G.
Biochem. Biophys. Res. Commun. 201, 493-499, 1994
A/Title: Mouse macrophage derived monocyte chemotactic protein-3: cDNA cloning and
A/Reference number: JC2452; MUID:94271193; PMID:8002978
A/Accession: JC2452
A/Molecule type: mRNA
A/Residues: 1-73, 'A', '75-97 <THI>
A/Cross-references: GB:S71251; NID:g547088; PIDN:AAB30997.1; PID:g547089
A/Experimental source: LPS-stimulated WEHI-3 cells
R/Kulmburg, P.A.; Huber, N.E.; Scheer, B.J.; Wrann, M.; Baumrucker, T.
J. Exp. Med. 176, 1773-1778, 1992
A/Title: Immunoglobulin E plus antigen challenge induces a novel intercrine/chemokine
A/Reference number: S30592; MUID:93094785; PMID:1281219
A/Accession: S30592
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-73, 'A', '75-97 <KUL>
A/Cross-references: EMBL:Z12297; NID:g57937; PIDN:CAA78169.1; PID:g57938
C/Genetics:
A/Gene: fic
C/Superfamily: macrophage inflammatory protein
C/Keywords: glycoprotein

F;29/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.0%; Score 244; DB 2; Length 97;
Best Local Similarity 51.5%; Pred. No. 1.5e-19;
Matches 51; Conservative 18; Mismatches 28; Indels 2; Gaps 2;

QY 11 MKVSALLCLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIQRLSEYTRITNIQCP 70
|::||| |||||:| | | ||| : |||: | :||| | | | :||
Db 1 MRISATLLCLLLIAAFSIQVWAQPDGPNAS-TCCY-VKKQKIPKRNLSYRRITSSRCP 58
QY 71 KEAVIFKTRKGKVCADPKERNVYRDSMKHLDQIFQNLKP 109
| ||||| |||:| | | : :||| : :| |
Db 59 WEAVIFKTKKGMEVCREAHQKWEAEAIAYLDMKTPTPKP 97

Search completed: February 18, 2003, 03:05:57
Job time : 41 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 18, 2003, 01:57:56 ; Search time 22 seconds
(without alignments)
205.496 Million cell updates/sec

Title: US-10-033-067-1
Perfect score: 567
Sequence: 1 MLKLTPLPSKMKVSALLCL.....ERWVRDSMKHLDQIFQNLKP 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	91.2	99	1	SY08_HUMAN P80075 homo sapien
2	382	67.4	99	1	SY02_MACFA Q9myn4 macaca fasc
3	372	65.6	99	1	SY08_PIG P49873 sus scrofa
4	367	64.7	99	1	SY02_HUMAN P13500 homo sapien
5	359	63.3	99	1	SY08_BOVIN Q09141 bos taurus
6	350	61.7	97	1	EOTA_HUMAN P51671 homo sapien
7	339	59.8	99	1	SY02_PIG P42831 sus scrofa
8	337	59.4	99	1	SY07_HUMAN P80098 homo sapien
9	328.5	57.9	98	1	SY13_HUMAN Q99616 homo sapien
10	327	57.7	101	1	SY02_CANFA P52203 canis famil
11	319.5	56.3	104	1	SY12_MOUSE Q62401 mus musculu
12	302	53.3	99	1	MCPA_BOVIN P28291 bos taurus
13	298	52.6	125	1	SY02_RABIT P28292 oryctolagus
14	283	49.9	97	1	EOTA_RAT P97545 rattus norv
15	282	49.7	97	1	SY08_MOUSE Q92121 mus musculu
16	280.5	49.5	96	1	EOTA_CAVPO P80325 cavia porce
17	270	47.6	97	1	EOTA_MOUSE P48298 mus musculu
18	259	45.7	148	1	SY02_MOUSE P10148 mus musculu
19	255	45.0	120	1	SY02_CAVPO Q08782 cavia porce
20	250	44.1	148	1	SY02_RAT P14844 rattus norv
21	249	43.9	97	1	SY07_MOUSE Q03366 mus musculu
22	239	42.2	74	1	MCPB_BOVIN P80343 bos taurus
23	239	42.2	97	1	SY07_RAT Q9qxy8 rattus norv
24	185.5	32.7	90	1	SY04_CHICK Q90826 gallus gail
25	183.5	32.4	93	1	SY3L_HUMAN P16619 homo sapien
26	174.5	30.8	92	1	SY04_HUMAN P13236 h small ind
27	172.5	30.4	119	1	SY24_MOUSE Q9jkc0 mus musculu
28	169.5	29.9	92	1	SY04_MOUSE P14097 mus musculu
29	169.5	29.9	92	1	SY04_RABIT P46632 oryctolagus
30	166.5	29.4	119	1	SY24_HUMAN Q00175 homo sapien
31	164.5	29.0	70	1	REG1_BOVIN P82943 bos taurus
32	163	28.7	91	1	SY05_CAVPO P97272 cavia porce
33	163	28.7	92	1	SY03_MOUSE P10855 mus musculu

ALIGNMENTS

34	162.5	28.7	92	1	SY04_RAT	P50230 rattus norv
35	159	28.0	92	1	SY03_HUMAN	P10147 homo sapien
36	158	27.9	92	1	SY03_RAT	P50229 rattus norv
37	157	27.7	91	1	SY05_HUMAN	P13501 homo sapien
38	156	27.5	91	1	SY05_BOVIN	Q97919 bos taurus
39	155	27.3	93	1	SY14_HUMAN	Q16627 homo sapien
40	149	26.3	91	1	SY05_MOUSE	P30882 mus musculu
41	148.5	26.2	120	1	SY16_HUMAN	O15467 h small ind
42	144	25.4	113	1	SY15_HUMAN	Q16663 homo sapien
43	140.5	24.8	120	1	SY23_HUMAN	P55773 homo sapien
44	139.5	24.6	92	1	SY05_RAT	P50231 rattus norv
45	136.5	24.1	96	1	SY01_HUMAN	P22362 homo sapien

RESULT 1
SY08_HUMAN
ID SY08_HUMAN STANDARD: PRT: 99 AA.
AC P80075: P78388;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic protein 2) (MCP-2) (Monocyte chemoattractant protein 2) (HC14).
GN SCYA8 OR SCYA10 OR MCP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., AND VARIANT GLN-69.
MEDLINE=97237052; PubMed=9119400;
RA van Collie E., Fiten P., Nomiya H., Sakaki Y., Miura R., Yoshie O., van Damme J., Opdenakker G.;
RT "The human MCP-2 gene (SCYA8): cloning, sequence analysis, tissue expression, and assignment to the CC chemokine gene contig on chromosome 17q11.2.";
RT Genomics 40:323-331(1997).
RL
[2]
SEQUENCE FROM N.A., AND VARIANT GLN-69.
TISSUE=Bone marrow;
RC MEDLINE=97224420; PubMed=9070881;
RA van Collie E., Froyen F., Nomiya H., Miura R., Fiten P., van Aelst I., van Damme J., Opdenakker G.;
RT "Human monocyte chemotactic protein-2: cDNA cloning and regulated expression of mRNA in mesenchymal cells.";
RT Biochem. Biophys. Res. Commun. 231:726-730(1997).
RL
[3]
SEQUENCE OF 23-99 FROM N.A.
MEDLINE=91207938; PubMed=2518726;
RA Chang H.C., Hsu F., Freeman G.J., Griffin J.D., Reinherz E.L.;
RT "Cloning and expression of a gamma-interferon-inducible gene in monocytes: a new member of a cytokine gene family.";
RT Int. Immunol. 1:388-399(1989).
RL
[4]
SEQUENCE OF 26-99.
TISSUE=Osteosarcoma;
RC MEDLINE=92308855; PubMed=1613466;
RA van Damme J., Proost P., Lenaerts J.-P., Opdenakker G.;
RT "Structural and functional identification of two human, tumor-derived monocyte chemotactic proteins (MCP-2 and MCP-3) belonging to the chemokine family.";
RT J. Exp. Med. 176:59-65(1992).
RL
[5]
SUBUNIT.
MEDLINE=97053697; PubMed=8898111;
RA Kim K.-S., Rajaratnam K., Clark-Lewis I., Sykes B.D.;
RT "Structural characterization of a monomeric chemokine: monocyte chemoattractant protein-3.";
RT FEBS Lett. 395:277-282(1996).
CC -!- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, LYMPHOCYTES,


```

CC BASOPHILS AND EOSINOPHILS. MAY PLAY A ROLE IN NEOPLASIA AND
CC INFLAMMATORY HOST RESPONSES. THIS PROTEIN CAN BIND HEPARIN.
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM.
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION FOUND IN THE SMALL
CC INTESTINE AND PERIPHERAL BLOOD CELLS. INTERMEDIATE LEVELS SEEN IN
CC THE HEART, PLACENTA, LUNG, SKELETAL MUSCLE, THYMUS, COLON, OVARY,
CC SPINAL CORD AND PANCREAS. LOW LEVELS SEEN IN THE BRAIN, LIVER,
CC SPLEEN AND PROSTATE.
CC -1- INDUCTION: BY INTERFERON GAMMA, MITOGENS AND INTERLEUKIN-1.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
DR EMBL; X99886; CAA68168.1; ALT_INIT.
DR EMBL; Y10802; CAA71760.1; -.
DR EMBL; Y16645; CAA76341.1; -.
DR HSSP; P51671; 1EOT.
DR Genew; HGNC:10635; SCYA8.
DR MIM; 602283; -.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
KW Polymorphism.
FT SIGNAL 1 23 PROBABLE.
FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A8.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
FT VARIANT 69 69 K -> Q.
FT FTID=VAR_001633.
SQ SEQUENCE 99 AA; 11246 MW; 9D67976BB9422F2A CRC64;

Query Match 91.2%; Score 517; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.6e-50;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MKVSAALLCLLLMAATFSPQGLAQPDSVSIPTCCFNVINRKIPIQRLSEYTRITNIQCP 70
Db 1 MKVSAALLCLLLMAATFSPQGLAQPDSVSIPTCCFNVINRKIPIQRLSEYTRITNIQCP 60

QY 71 KEAVIFKTRKGKVCADPKERWVRDSMKHLDOIIFQNLKP 109
Db 61 KEAVIFKTRKGKVCADPKERWVRDSMKHLDOIIFQNLKP 99

RESULT 2
SY02_MACFA STANDARD; PRT; 99 AA.
ID SY02_MACFA
AC O9MYN4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN SCYA2 OR MCP1.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9541, 9544;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC SPECIES=M.fascicularis;
RA Studer C., Ufer R.;
RT "Cloning and expression of cynomolgus monkey chemoattractant
RT protein-1.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RA Studer C., Ufer R.;
RT "Cloning and expression of rhesus monkey monocyte chemoattractant
RT protein-1.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES AND BASOPHILS
CC BUT NOT NEUTROPHILS OR EOSINOPHILS. BINDS TO CCR2 AND CCR4 (BY
CC SIMILARITY).
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
DR EMBL; AF276081; AAF81899.1; -.
DR EMBL; AF255343; AAF67756.1; -.
DR HSSP; P13500; 1DOK.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 99 AA; 11007 MW; 433CB88C64E7A4F CRC64;

Query Match 67.4%; Score 382; DB 1; Length 99;
Best Local Similarity 70.7%; Pred. No. 1.5e-35;
Matches 70; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 11 MKVSAALLCLLLMAATFSPQGLAQPDSVSIPTCCFNVINRKIPIQRLSEYTRITNIQCP 70
Db 1 MKVSAALLCLLLMAATFSPQGLAQPDAINAPVTCYNTNRKISVQRLASYRRITSSKCP 60

QY 71 KEAVIFKTRKGKVCADPKERWVRDSMKHLDOIIFQNLKP 109
Db 61 KEAVIFKTRKGEICADPKOKWQDSMDHLDOIIFQNP 99

RESULT 3
SY08_PIG STANDARD; PRT; 99 AA.
ID SY08_PIG
AC P49873;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
GN SCYA8 OR MCP2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95091716; PubMed-7999015;
RA Hosang K.K., Knoke I.I., Klaudiny J.J., Wempe F.F., Wuttke W.W.,
RT Scheit K.K.;
RL "Porcine luteal cells express monocyte chemoattractant protein-2
(MCP-2): analysis by cDNA cloning and northern analysis.";
CC Biochem. Biophys. Res. Commun. 205:148-153(1994).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES. THIS PROTEIN
CC CAN BIND HEPARIN.
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
CC EMBL; Z48480; CAA88371.1; -.
DR DR HSSP; P51671; 1EOT.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A8.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 34 59 BY SIMILARITY.
FT FT 35 75 BY SIMILARITY.
SQ SEQUENCE 99 AA; 10903 MW; D3DAA0F7A964CDB1 CRC64;

Query Match 65.6%; Score 372; DB 1; Length 99;
Best Local Similarity 72.7%; Pred. No. 1.9e-34;
Matches 72; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 11 MKVSALLCLLMAATFSPQGLAOPDSVSIPTCCFVNRKIPQRLSYTRITNIQCP 70
|:||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MOVSALLCLLTTAFTSTQVLAQPDVSIPITCCFGLVNGKIPFKLLESTYRITNSQCP 60

QY 71 KEAVIFKTKRGEVCAADPKERWVRDSMKHLDIQNLKP 109
:||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 QEAVIFKTKADKEVCADPQQKWNQNSMKLLDQKSQTPKP 99

RESULT 4
SY02_HUMAN
ID SY02_HUMAN STANDARD; PRT; 99 AA.
AC P13500; Q9UDF3;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1) (Monocyte
DE chemotactic and activating factor) (MCAF) (Monocyte secretory protein
DE JE) (HC11).
GN SCYA2 OR MCP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89165862; PubMed=2923622;
RA Furutani Y., Nomura H., Notake M., Oyama Y., Fukui T., Yamada M.,
RA Larsen C.G., Oppenheim J.J., Matsushima K.;
RT "Cloning and sequencing of the cDNA for human monocyte chemotactic

```

RT and activating factor (MCAF).";
RL Biochem. Biophys. Res. Commun. 159:249-255(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90097880; PubMed=2513477;
RA Rollins B.J., Stier P., Ernst T., Wong G.G.;
RT "The human homolog of the JE gene encodes a monocyte secretory
RL protein.";
RN Mol. Cell. Biol. 9:4687-4695(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89153605; PubMed=2465924;
RA Yoshimura T., Yuhki N., Moore S.K., Appella E., Lerman M.I.,
RA Leonard E.J.;
RT "Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA
RT cloning, expression in mitogen-stimulated blood mononuclear
RT leukocytes, and sequence similarity to mouse competence gene JE.";
RL FEBS Lett. 244:487-493(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90290466; PubMed=2357211;
RA Shyy Y.J., Li Y.S., Kolattukudy P.E.;
RT "Structure of human monocyte chemotactic protein gene and its
RT regulation by TPA.";
RL Biochem. Biophys. Res. Commun. 169:346-351(1990).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=91207938; PubMed=2518726;
RA Chang H.C., Hsu F., Freeman G.J., Griffin J.D., Reinherz E.L.;
RT "Cloning and expression of a gamma-interferon-inducible gene in
RT monocytes: a new member of a cytokine gene family.";
RL Int. Immunol. 1:388-399(1989).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150478; PubMed=8107690;
RA Li Y.S., Shyy Y.J., Wright J.G., Valente A.J., Cornhill J.F.,
RA Kolattukudy P.E.;
RT "The expression of monocyte chemotactic protein (MCP-1) in human
RT vascular endothelium in vitro and in vivo.";
RL Mol. Cell. Biochem. 126:61-68(1993).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=92095166; PubMed=1661560;
RA Yoshimura T., Leonard E.J.;
RT "Human monocyte chemoattractant protein-1 (MCP-1).";
RL Adv. Exp. Med. Biol. 305:47-56(1991).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=91301709; PubMed=2071154;
RA Rollins B.J., Morton C.C., Ledbetter D.H., Eddy R.L. Jr., Shows T.B.
RT "Assignment of the human small inducible cytokine A2 gene, SCYA2
RT (encoding JE or MCP-1), to 17q11.2-12: evolutionary relatedness of
RL cytokines clustered at the same locus.";
RN Genomics 10:489-492(1991).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=20374005; PubMed=10918580;
RA Finer P., Soto U., Delius H., Patzelt A., Poustka A., Coy J.F.,
RA zur Hausen H., Roese F.;
RT "Differential transcriptional regulation of the
RT monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and
RT non-tumorigenic HPV 18 positive cells: The role of the chromatin
RL structure and AP-1 composition.";
RN Oncogene 19:3235-3244(2000).
RN [10]
RP SEQUENCE OF 24-99.
RX MEDLINE=89184525; PubMed=2648385;
RA Robinson E.A., Yoshimura T., Leonard E.J., Tanaka S., Griffin P.R.,
RA Shabanowitz J., Hunt D.F., Appella E.;
RT "Complete amino acid sequence of a human monocyte chemoattractant, a
RT putative mediator of cellular immune reactions.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1850-1854(1989).
RN [11]

RP SEQUENCE OF 29-53 AND 82-92.
RX MEDLINE=90211336; PubMed=2322286;
RA Decock B., Conings R., Lenaerts J.-P., Billiau A., van Damme J.;
RT "Identification of the monocytic chemotactic protein from human
RT osteosarcoma cells and monocytes: detection of a novel N-terminally
RT processed form.";
RL Biochem. Biophys. Res. Commun. 167:904-909(1990).
RN [12]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=91312872; PubMed=1857712;
RA Gronenborn A.M., Clore G.M.;
RT "Modeling the three-dimensional structure of the monocyte chemo-
RT attractant and activating protein MCAF/MCP-1 on the basis of the
RT solution structure of interleukin-8.";
RL Protein Eng. 4:263-269(1991).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=97143315; PubMed=8989326;
RA Lubkowski J., Bujacz G., Domaille P.J., Handel T.M., Wlodawer A.;
RT "The structure of MCP-1 in two crystal forms provides a rare example
RT of variable quaternary interactions.";
RL Nat. Struct. Biol. 4:64-69(1997).
RN [14]
RP STRUCTURE BY NMR.
RX MEDLINE=96234959; PubMed=8639605;
RA Handel T.M., Domaille P.J.;
RT "Heteronuclear ¹H, ¹³C, ¹⁵N) NMR assignments and solution structure
RT of the monocyte chemoattractant protein-1 (MCP-1) dimer.";
RL Biochemistry 35:6569-6584(1996).
RN [15]
RP EFFECT OF DELETION OF N-TERMINAL RESIDUES.
RX MEDLINE=96195223; PubMed=8627182;
RA Weber M., Ugucioni M., Baggiolini M., Clark-Lewis I., Dahinden C.A.;
RT "Deletion of the NH2-terminal residue converts monocyte chemotactic
RT protein 1 from an activator of basophil mediator release to an
RT eosinophil chemoattractant.";
RL J. Exp. Med. 183:681-685(1996).
RN [16]
RP MUTAGENESIS.
RX MEDLINE=94253189; PubMed=8195247;
RA Zhang Y.J., Rutledge B.J., Rollins B.J.;
RT "Structure/activity analysis of human monocyte chemoattractant
RT protein-1 (MCP-1) by mutagenesis. Identification of a mutated protein
RT that inhibits MCP-1-mediated monocyte chemotaxis.";
RL J. Biol. Chem. 269:15918-15924(1994).
RN [17]
RP SUBUNIT.
RX MEDLINE=97053697; PubMed=8898111;
RA Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.;
RT "Structural characterization of a monomeric chemokine: monocyte
RT chemoattractant protein-3.";
RL FEBS Lett. 395:277-282(1996).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES AND BASOPHILS
CC BUT NOT NEUTROPHILS OR EOSINOPHILS. AUGMENTS MONOCYTE ANTI-TUMOR
CC ACTIVITY. HAS BEEN IMPLICATED IN THE PATHOGENESIS OF DISEASES
CC CHARACTERIZED BY MONOCYTIC INFILTRATES, LIKE PSORIASIS, RHEUMATOID
CC ARTHRITIS OR ATHEROSCLEROSIS. MAY BE INVOLVED IN THE RECRUITMENT
CC OF MONOCYTES INTO THE ARTERIAL WALL DURING THE DISEASE PROCESS OF
CC ATHEROSCLEROSIS. BINDS TO CCR2 AND CCR4.
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: PROCESSING AT THE N-TERMINUS CAN REGULATE RECEPTOR AND TARGET
CC CELL SELECTIVITY. DELETION OF THE N-TERMINAL RESIDUE CONVERTS
CC IT FROM AN ACTIVATOR OF BASOPHIL TO AN EOSINOPHIL CHEMOATTRACTANT.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
DR EMBL; M31626; AAA36330.1; -
DR EMBL; M30816; AAA36330.1; JOINED.
DR EMBL; M31625; AAA36330.1; JOINED.
DR EMBL; M24545; AAA18164.1; -
DR EMBL; M28226; AAA60309.1; -
DR EMBL; M37719; AAA18102.1; -
DR EMBL; M28225; AAA60308.1; -
DR EMBL; M28223; AAA60308.1; JOINED.
DR EMBL; M28224; AAA60308.1; JOINED.
DR EMBL; S69738; AAB29926.1; -
DR EMBL; S71513; AAB20651.1; -
DR EMBL; Y18933; CAC14049.1; -
DR EMBL; A17786; CAA01352.1; -
DR PIR; A35474; A35474.
DR PIR; S03339; S03339.
DR PDB; 1DOK; 12-MAR-97.
DR PDB; 1DOL; 12-MAR-97.
DR PDB; 1DOM; 14-OCT-96.
DR PDB; 1DON; 14-OCT-96.
DR PDB; 1MCA; 15-OCT-94.
DR Genew; HGNC:10618; SCYA2.
DR MIM; 158105; -
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.

Query Match 64.7%; Score 367; DB 1; Length 99;
Best Local Similarity 69.4%; Pred. No. 6.9e-34;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 11 MKVSALLCLLMAATFSPQGLAQPDSVSIPTCCFNVINRKIPQRLSEYTRTNIQCP 70
Db 1 MKVSALLCLLLIATFIPQGLAQPDAINAPVTCYNTNRKISVQRLASTRTSSKCP 60

QY 71 KEAVIFKTKGKEVCADPKERWVRDMSMKHLDFQNLK 108
Db 61 KEAVIFKTIYAKKICADPKQKWQDSMDHLDKQTQTPK 98

RESULT 5
SY08_BOVIN STANDARD; PRT; 99 AA.
ID SY08_BOVIN
AC 009141;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
GN SCYA8 OR MCP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94114084; PubMed=8286035;
RA Wempe F., Hanes J., Scheit K.H.;
RT "Cloning of the gene for bovine monocyte chemoattractant protein-2.";
RL DNA Cell Biol. 13:1-8(1994).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES. THIS PROTEIN
CC CAN BIND HEPARIN.
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE


```
CC C-C) (CHEMOKINE CC).
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S67954; AAD14005.1; -.
DR EMBL; S67956; AAB29750.1; -.
DR HSSP; P51671; 1EOT.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A8.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
SQ SEQUENCE 99 AA; 10900 MW; 01974CDB3FF9119B CRC64;

Query Match 63.3%; Score 359; DB 1; Length 99;
Best Local Similarity 68.7%; Pred. No. 5.3e-33;
Matches 68; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 11 MKVSALLCLLMATFSPQGLAOPDSVSIPTCCFNVINRKIPQRLSEYRTNIGCP 70
    |||||:|||||:||||| |||||:||||| ||| :||:||||| |||
Db 1 MKVSAGILCLLVATFGTQVLAQPDVSSTPTCCFSVINGKIPEKLDSTYRTNIGCP 60

QY 71 KEAVIFKTRKRGKVCADPKERWVRDSMKHLQIFQNLKP 109
    :|||||:|||||:|||||: ||| :|||
Db 61 OEAVIFKTRKADRDVCAADPKQKVVQTSIRLLDQKSRTPKP 99

RESULT 6
EOTA_HUMAN
ID EOTA_HUMAN STANDARD; PRT; 97 AA.
AC P51671; P50877; Q92490; Q92491;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Eotaxin precursor (Small inducible cytokine A11) (CCL11) (Eosinophil
DE chemotactic protein).
GN SCYA11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96181758; Pubmed=8597956;
RA Garcia-Zepeda E.A., Rothenberg M.E., Ownbey T.R., Leder P.,
RA Luster A.D.;
RT "Human eotaxin is a specific chemoattractant for eosinophil cells and
RT provides a new mechanism to explain tissue eosinophilia.";
RL Nat. Med. 2:449-456(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96189937; Pubmed=8609214;
RA Ponath P.D., Qin S., Ringler D.J., Clark-Lewis I., Wang J., Kassam N.,
RA Smith H., Shi X., Gonzalo J.A., Newman W., Gutierrez-Ramos J.C.,
RA Mackay C.R.;
RT "Cloning of the human eosinophil chemoattractant, eotaxin. Expression,
RT receptor binding, and functional properties suggest a mechanism for
RT the selective recruitment of eosinophils.";
RL J. Clin. Invest. 97:604-612(1996).
RN [3]

RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96205964; Pubmed=8631813;
RA Kitaura M., Nakajima T., Imai T., Harada S., Combadiere C.,
RA Tiffany H.L., Murphy P.M., Yoshie O.;
RT "Molecular cloning of human eotaxin, an eosinophil-selective CC
RT chemokine, and identification of a specific eosinophil eotaxin
RT receptor, CC chemokine receptor 3.";
RL J. Biol. Chem. 271:7725-7730(1996).
RN [4]
RP SEQUENCE FROM N.A., SEQUENCE OF 60-65 AND 75-88, AND VARIANTS.
RC TISSUE=Foreskin;
RX MEDLINE=96374440; Pubmed=8780731;
RA Bartels J., Schlueter C., Richter E., Noso N., Kulke R.,
RA Christophers E., Schroeder J.M.;
RT "Human dermal fibroblasts express eotaxin: molecular cloning, mRNA
RT expression, and identification of eotaxin sequence variants.";
RL Biochem. Biophys. Res. Commun. 225:1045-1051(1996).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97312708; Pubmed=9169149;
RA Garcia-Zepeda E.A., Rothenberg M.E., Weremowicz S., Sarafi M.N.,
RA Morton C.C., Luster A.D.;
RT "Genomic organization, complete sequence, and chromosomal location of
RT the gene for human eotaxin (SCYA11), an eosinophil-specific CC
RT chemokine.";
RL Genomics 41:471-476(1997).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=97445071; Pubmed=9239399;
RA Hein H., Schlueter C., Kulke R., Christophers E., Schroeder J.M.,
RA Bartels J.;
RT "Genomic organization, sequence, and transcriptional regulation of
RT the human eotaxin gene.";
RL Biochem. Biophys. Res. Commun. 237:537-542(1997).
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP CARBOHYDRATE-LINKAGE SITE.
RC TISSUE=Blood;
RX MEDLINE=98237580; Pubmed=9578468;
RA Noso N., Bartels J., Mallet A.I., Mochizuki M., Christophers E.,
RA Schroeder J.-M.;
RT "Delayed production of biologically active O-glycosylated forms of
RT human eotaxin by tumor-necrosis-factor-alpha-stimulated dermal
RT fibroblasts.";
RL Eur. J. Biochem. 253:114-122(1998).
RN [9]
RP STRUCTURE BY NMR.
RX MEDLINE=98380469; Pubmed=9712872;
RA Crump M.P., Rajarathnam K., Kim K.S., Clark-Lewis I., Sykes B.D.;
RT "Solution structure of eotaxin, a chemokine that selectively recruits
RT eosinophils in allergic inflammation.";
RL J. Biol. Chem. 273:22471-22479(1998).
CC -I- FUNCTION: IN RESPONSE TO THE PRESENCE OF ALLERGENS, THIS PROTEIN
CC DIRECTLY PROMOTES THE ACCUMULATION OF EOSINOPHILS, A PROMINENT
CC FEATURE OF ALLERGIC INFLAMMATORY REACTIONS. BINDS TO CCR3.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- INDUCTION: BY TNF-ALPHA, INTERLEUKIN-1 ALPHA AND INTERFERON GAMMA.
CC -I- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE WHICH
CC IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES.
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -I- DATABASE: NAME=R&D Systems' cytokine source book: SCYA11;
CC WWW="http://www.rndsystems.com/asp/g_9-sitebuilder.asp?bodyId=196".
CC -----
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DR EMBL: U46573; AAA98957.1; -
DR EMBL: U34780; AAC50369.1; -
DR EMBL: D49372; BAA08370.1; -
DR EMBL: Z69291; CAA93258.1; -
DR EMBL: Z75668; CAA99997.1; -
DR EMBL: Z75669; CAA99998.1; -
DR EMBL: U46572; AAC51297.1; -
DR EMBL: Z92709; CAB07027.1; -
DR EMBL: BC017850; AAH17850.1; -
DR PDB: 1EOT; 13-JAN-99.
DR PDB: 2EOT; 11-NOV-98.
DR Genew; HGNC:10610; SCYA11.
DR MIM: 601156; -
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Eosinophil; Cytokine; Chemotaxis; Glycoprotein; Signal;
KW Inflammatory response; Polymorphism; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 97 EOTAXIN.
FT DISULFID 32 57
FT DISULFID 33 73
FT CARBOHYD 94 94
FT VARIANT 7 7
FT VARIANT 23 23
FT VARIANT 51 51
FT VARIANT 79 79
SQ SEQUENCE 97 AA; 10732 MW; B433C30FDA4C71A7 CRC64;
Query Match 61.7%; Score 350; DB 1; Length 97;
Best Local Similarity 68.7%; Pred. No. 5.2e-32;
Matches 68; Conservative 14; Mismatches 15; Indels 2; Gaps 1;
QY 11 MKVSALLCLLLMAATFSPQGLAOPDSVIPITCCFNVINRKIPIQRLSYTRITNIQCP 70
11 MKVSALLCLLLMAATFSPQGLAOPDSVIPITCCFNVINRKIPIQRLSYTRITNIQCP 70
DB 1 MKVSALLCLLLMAATFSPQGLAOPDSVIPITCCFNVINRKIPIQRLSYTRITNIQCP 58
QY 71 KEAVIFKTRGKEVCADPKERWVRDSMKHLDOIIFQNLKP 109
71 KEAVIFKTRGKEVCADPKERWVRDSMKHLDOIIFQNLKP 109
DB 59 QKAVIFKTKLAKDICADPKKKWQDSMKYIDQKSPTPKP 97
RESULT 7
SY02_PIG STANDARD; PRT; 99 AA.
ID SY02_PIG
AC P42831;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A2 precursor (CCIL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN SCYA2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94183284; PubMed=7510962;
RA Hosang K., Knoke I., Klaudiny J., Wempe F., Muttke W., Scheit K.H.;
RT "Porcine luteal cells express monocyte chemoattractant protein-1

RP (MCP-1): analysis by polymerase chain reaction and cDNA cloning.";
RL Biochem. Biophys. Res. Commun. 199:962-968(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Zach O.R.F.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
CC NEUTROPHILS.
CC -!- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).

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DR EMBL: Z48479; CAA88370.1; -
DR EMBL: X79416; CAA55945.1; -
DR HSSP; P13500; IDOM.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response.
FT SIGNAL 1 23
FT CHAIN 24 99
FT MOD_RES 24 24
FT DISULFID 34 59
FT DISULFID 35 75
SQ SEQUENCE 99 AA; 10976 MW; 4C0AC627BD4F0A09 CRC64;
Query Match 59.8%; Score 339; DB 1; Length 99;
Best Local Similarity 62.6%; Pred. No. 8.7e-31;
Matches 62; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
QY 11 MKVSALLCLLLMAATFSPQGLAOPDSVIPITCCFNVINRKIPIQRLSYTRITNIQCP 70
11 MKVSALLCLLLMAATFSPQGLAOPDSVIPITCCFNVINRKIPIQRLSYTRITNIQCP 70
DB 1 MKVSALLCLLLMAATFSPQGLAOPDSVIPITCCFNVINRKIPIQRLSYTRITNIQCP 60
QY 71 KEAVIFKTRGKEVCADPKERWVRDSMKHLDOIIFQNLKP 109
71 KEAVIFKTRGKEVCADPKERWVRDSMKHLDOIIFQNLKP 109
DB 61 KEAVIFKTKAGKEICAEPRQKWQDSISHLDKKNQTPKP 99
RESULT 8
SY07_HUMAN STANDARD; PRT; 99 AA.
ID SY07_HUMAN
AC P80098;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A7 precursor (CCIL7) (Monocyte chemotactic
DE protein 3) (MCP-3) (Monocyte chemoattractant protein 3) (NC28).
GN SCYA7 OR MCP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-67 AND 71-99.
RX MEDLINE=93213290; PubMed=8461011;
RA Opdenakker G., Froyen G., Fiten P., Proost P., van Damme J.;
RT "Human monocyte chemotactic protein-3 (MCP-3): molecular cloning of
RL the cDNA and comparison with other chemokines.";
Biochem. Biophys. Res. Commun. 191:535-542(1993).

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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94375065; PubMed=7916328;
RA Opdenakker G., Fiten P., Nys G., Froyen G., van Roy N., Speleman F.,
RA Laureys G., van Damme J.;
RT "The human MCP-3 gene (SCYA7): cloning, sequence analysis, and
RT assignment to the C-C chemokine gene cluster on chromosome
RT 17q11.2-q12.";
RL Genomics 21:403-408(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93305913; PubMed=8318676;
RA Minty A., Chalou P., Guillemot J.C., Kaghad M., Liauzun P.,
RA Magazin M., Miloux B., Minty C., Ramond P., Vita N., Lupker J.,
RA Shire D., Ferrara P., Caput D.;
RT "Molecular cloning of the MCP-3 chemokine gene and regulation of its
RT expression.";
RL Eur. Cytokine Netw. 4:99-110(1993).
RN [4]
RP SEQUENCE OF 24-99 FROM N.A.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 30-99.
RC TISSUE=Osteosarcoma;
RX MEDLINE=92308855; PubMed=1613466;
RA van Damme J., Proost P., Lenaerts J.-P., Opdenakker G.;
RT "Structural and functional identification of two human, tumor-derived
RT monocyte chemotactic proteins (MCP-2 and MCP-3) belonging to the
RT chemokine family.";
RL J. Exp. Med. 176:59-65(1992).
RN [6]
RP STRUCTURE BY NMR, AND SUBUNIT.
RX MEDLINE=97053697; PubMed=8898111;
RA Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.;
RT "Structural characterization of a monomeric chemokine: monocyte
RT chemoattractant protein-3.";
RL FEBS Lett. 395:277-282(1996).
RN [7]
RP STRUCTURE BY NMR.
RX MEDLINE=97263733; PubMed=9109648;
RA Meunier S., Bernassau J.-M., Guillemot J.-C., Ferrara P., Darbon H.;
RT "Determination of the three-dimensional structure of CC chemokine
RT monocyte chemoattractant protein 3 by 1H two-dimensional NMR
RT spectroscopy.";
RL Biochemistry 36:4412-4422(1997).
RN [8]
RP STRUCTURE BY NMR.
RA Kwon D., Lee D., Sykes B.D., Kim K.-S.;
RL Submitted (AUG-1998) to the PDB data bank.
CC -!- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES AND
CC EOSINOPHILS, BUT NOT NEUTROPHILS. AUGMENTS MONOCYTE ANTI-TUMOR
CC ACTIVITY. ALSO INDUCES THE RELEASE OF GELATINASE B. THIS PROTEIN
CC CAN BIND HEPARIN. BINDS TO CCR1, CCR2 AND CCR3.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: O-GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
DR EMBL; X72308; CAA51055.1; ALT_INIT.
DR EMBL; X72309; -: NOT_ANNOTATED_CDS.
DR EMBL; X71087; CAA50407.1; -.
DR EMBL; X71087; CAA50406.1; ALT_INIT.
DR EMBL; X71087; CAA50405.1; ALT_INIT.

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DR EMBL; AF043338; AAC03538.1; -.
DR PIR; JC1478; JC1478.
DR PIR; S32222; S32222.
DR PIR; A54678; A54678.
DR PDB; 1NCV; 15-OCT-97.
DR PDB; 1BO0; 10-OCT-99.
DR Genew; HGNC:10634; SCYA7.
DR MIM; 158106; -.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Heparin-binding; Glycoprotein; Signal;
KW Inflammatory response; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 1 24 99
FT MOD_RES 24 24 24
FT DISULFID 34 59
FT DISULFID 35 75
FT CARBOHYD 29 29
FT CONFLICT 30 30
FT CONFLICT 68 70
SQ SEQUENCE 99 AA; 11200 MW; 96048B371C25D00E CRC64;
Query Match 59.4%; Score 337; DB 1; Length 99;
Best Local Similarity 65.3%; Pred. No. 1.5e-30;
Matches 64; Conservative 11; Mismatches 23; Indels 0; Gaps 0;
QY 11 MKVSALLCLLMAATFSPQGLAQPDSVIPITCCFNVNKRKIPQRLSEYTRITNOCF 70
Db 1 MKASALLCLLLTAAPFSPQGLAQPVGINTSTCCYRINKKIPKORLESYRRITSSHCP 60
QY 71 KEAVIFKTKRGKEVCADPKERWVRDSMKHLDFQNLK 108
Db 61 REAVIFKTKLKDKEICADPTQKWVDFMKHLDKKTQTPK 98
RESULT 9
SY13_HUMAN
ID SY13_HUMAN STANDARD; PRT; 98 AA.
AC Q99616;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A13 precursor (CCL13) (Monocyte chemotactic
DE protein 4) (MCP-4) (Monocyte chemoattractant protein 4) (CK-beta-10)
DE (MCC-1).
GN SCYA13 OR MCP4 OR NCC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=97113354; PubMed=8955214;
RA Garcia-Zepeda E.A., Combadiere C., Rothenberg M.E., Sarafi M.N.,
RA Lavigne F., Hamid Q., Murphy P.M., Luster A.D.;
RT "Human monocyte chemoattractant protein (MCP)-4 is a novel CC
RT chemokine with activities on monocytes, eosinophils, and basophils
RT induced in allergic and nonallergic inflammation that signals through
RT the CC chemokine receptors (CCR)-2 and -3.";
RL J. Immunol. 157:5613-5626(1996).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 17-98.
RC TISSUE=Fetal;
RX MEDLINE=96235049; PubMed=8642349;
RA Uguccioni M., Loetscher P., Forssmann U., Dewald B., Li H., Lima S.H.,
RA Li Y., Kreider B., Garotta G., Thelen M., Baggiolini M.;
RT "Monocyte chemotactic protein 4 (MCP-4), a novel structural and
RT functional analogue of MCP-3 and eotaxin.";
RL J. Exp. Med. 183:2379-2384(1996).

```

RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-33.
RC TISSUE-Fetal;
RX MEDLINE=97341179; PubMed=9195948;
RA Berkhout T.A., Sarau H.M., Moores K., White J.R., Elshourbagy N.,
RA Appelbaum E., Reape T.J., Brawner M., Makwana J., Foley J.J.,
RA Schmidt D.B., Imburgia C., Macnulty D., Matthews J., O'Donnell K.,
RA O'Shannessy D., Scott M., Groot P.H.E., Macphee C.;
RT "Cloning, in vitro expression, and functional characterization of a
RT novel human CC chemokine of the monocyte chemotactic protein (MCP)
RT family (MCP-4) that binds and signals through the CC chemokine
RT receptor 2B.";
RL J. Biol. Chem. 272:16404-16413(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Dante M., Gibson A.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Power C.A., Meyer A., Rison S.C.G., Guye-Coulin F., Wells T.N.C.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=97213770; PubMed=9060459;
RA Godiska R., Chantry D., Raport C.J., Schweickart V.L., Trong H.L.,
RA Gray P.W.;
RT "Monocyte chemotactic protein-4: tissue-specific expression and
RT signaling through CC chemokine receptor-2.";
RL J. Leukoc. Biol. 61:353-360(1997).
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin fibroblast;
RX MEDLINE=99160888; PubMed=10049733;
RA Hein H., Schluter C., Kulke R., Christophers E., Schroder J.M.,
RA Bartels J.;
RT "Genomic organization, sequence analysis and transcriptional
RT regulation of the human MCP-4 chemokine gene (SCYA13) in dermal
RT fibroblasts: a comparison to other eosinophilic beta-chemokines.";
RL Biochem. Biophys. Res. Commun. 255:470-476(1999).
RN [8]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, LYMPHOCYTES,
CC BASOPHILS AND EOSINOPHILS, BUT NOT NEUTROPHILS. SIGNALS THROUGH
CC CCR2B AND CCR3 RECEPTORS. PLAYS A ROLE IN THE ACCUMULATION OF
CC LEUKOCYTES AT BOTH SIDES OF ALLERGIC AND NONALLERGIC INFLAMMATION.
CC MAY BE INVOLVED IN THE RECRUITMENT OF MONOCYTES INTO THE ARTERIAL
CC WALL DURING THE DISEASE PROCESS OF ARTEROSCLEROSIS. MAY PLAY A
CC ROLE IN THE MONOCYTE ATTRACTION IN TISSUES CHRONICALLY EXPOSED TO
CC EXOGENOUS PATHOGENS.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: WIDELY EXPRESSED. FOUND IN SMALL INTESTINE,
CC THYMUS, COLON, LUNG, TRACHEA, STOMACH AND LYMPH NODE. LOW LEVELS
CC SEEN IN THE PULMONARY ARTERY SMOOTH MUSCLE CELLS.
CC -I- INDUCTION: BY INTERLEUKIN-1 AND TNF-ALPHA.
CC -I- PTM: ONE MAJOR ISOFORM MCP-4, AND TWO MINOR ISOFORMS (LA)MCP-4 AND
CC (LA)MCP-4 ARE PRODUCED BY DIFFERENTIAL SIGNAL CLEAVAGE.
CC (LA)MCP-4 IS ABOUT 30 FOLD LESS ACTIVE THAN MCP-4.
CC -I- MASS SPECTROMETRY: MW=9314; MW_ERR=30; METHOD=MALDI; RANGE=17-98.
CC -I- MASS SPECTROMETRY: MW=8760; MW_ERR=30; METHOD=MALDI; RANGE=22-98.
CC -I- MASS SPECTROMETRY: MW=8575; MW_ERR=30; METHOD=MALDI; RANGE=24-98.
CC -I- MISCELLANEOUS: THIS PROTEIN CAN BIND HEPARIN.
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).

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DR EMBL; U46767; AAB38703.1; -.
DR EMBL; AC002482; AAB67307.1; -.
DR EMBL; X98306; CAA66950.1; -.
DR EMBL; U59808; AAD09362.1; -.
DR EMBL; AJ001634; CAA04888.1; -.
DR EMBL; BC008621; AAH08621.1; -.
DR HSSP; P51671; 1EOT.
DR Genew; HGNC:10611; SCYA13.
DR MIM; 601391; -.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Glycoprotein; Inflammatory response.
FT SIGNAL 1 16
FT CHAIN 17 98 SMALL INDUCIBLE CYTOKINE A13, LONG FORM.
FT CHAIN 24 98 SMALL INDUCIBLE CYTOKINE A13, SHORT FORM.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 34 58 BY SIMILARITY.
FT DISULFID 35 74 BY SIMILARITY.
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 98 AA; 10986 MW; 612688DFCD308873 CRC64;

Query Match 57.9%; Score 328.5; DB 1; Length 98;
Best Local Similarity 62.2%; Pred. No. 1.3e-29;
Matches 61; Conservative 18; Mismatches 18; Indels 1; Gaps 1;

QY 11 MKVSAALICLLMAATFSPQGLAOPDSVSTPTCCFNVINKRPIQRLESTRTINIQCP 70
Db 1 MKVSAVLCLLLMTAAFPQGLAOPDALNVSTCCFTFSSKSKISLRKSYV-ITTSRCP 59

QY 71 KEAVIFKTRKGEVCADPKERWVRDSMKHLDOIIONLK 108
Db 60 OKAVIFRTKLGKEICADPKERWQNYMKHLGRKAHTLK 97

RESULT 10
SY02_CANFA
ID SY02_CANFA STANDARD; PRT; 101 AA.
AC P52203;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN SCYA2 OR MCP1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Jugular vein endothelial;
RX MEDLINE=97176620; PubMed=9024159;
RA Kumar A.G., Ballantyne C.M., Michael L.H., Kukiela G.L., Youker K.A.,
RA Lindsey M.L., Hawkins H.K., Birdsell H.H., Mackay C.R., Larosa G.J.,
RA Rossen R.D., Smith C.W., Entman M.L.;
RT "Induction of monocyte chemoattractant protein-1 in the small veins
RT of the ischemic and reperfused canine myocardium.";
RL Circulation 95:693-700(1997).
CC -I- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
CC NEUTROPHILS. IMPORTANT FACTOR IN THE COURSE OF THE INFLAMMATORY
CC REACTION TO REPERFUSION OF THE PREVIOUSLY ISCHEMIC MYOCARDIUM.
CC MAY PLAY A SIGNIFICANT ROLE IN MONOCYTE TRAFFICKING INTO THE
CC REPERFUSED MYOCARDIUM.
CC -I- SUBUNIT: MONOMER OR HOMODIMER, IN EQUILIBRIUM (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: ENDOTHELIUM OF SMALL VEINS AND INTRAFASCICULAR
CC VEINS, AND INFILTRATING LEUKOCYTES.


```
CC -I- INDUCTION: BY TNF-ALPHA.
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
-----
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CC EMBL; U29653; AAA84911.1; -.
CC HSSP; P13500; 1DOM.
CC InterPro: IPR000827; CC_chemkine.sml.
CC InterPro: IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CC Cytokine; Chemotaxis; Signal; Inflammatory response.
CC SIGNAL 1 23 BY SIMILARITY.
CC CHAIN 24 101 SMALL INDUCIBLE CYTOKINE A2.
CC MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
CC SIMILARITY).
CC DISULFID 34 59 BY SIMILARITY.
CC DISULFID 35 75 BY SIMILARITY.
CC SEQUENCE 101 AA; 11121 MW; CDD7E2B1901A7267 CRC64;

Query Match 57.7%; Score 327; DB 1; Length 101;
Best Local Similarity 64.1%; Pred. No. 1.9e-29;
Matches 59; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 11 MKVSALLCLLMAATFSPQGLAOPDSVSIPITCCFENVINRKIPQRLSEYTRITNIQCP 70
    |||||
Db 1 MKVSALLCLLLIAAALTTOVLTPDAISPVTCCTLTNKKISIQRLASYKRVTSKCP 60
    |||||

QY 71 KEAVIFKTRGKEVCADPKERWVRDSMKHLDO 102
    |||||
Db 61 KEAVIFKTVLNKEICADPKQKWQDSMAHLDR 92

RESULT 11
SY12_MOUSE STANDARD; PRT; 104 AA.
ID SY12_MOUSE STANDARD; PRT; 104 AA.
AC 062401; 09QYD6;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A12 precursor (CCL12) (monocyte chemotactic
DE protein 5) (MCP-5) (MCP-1 related chemokine).
GN SCYA12 OR MCP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97079149; PubMed=8920881;
RA Jia G.-Q., Gonzalo J.A., Lloyd C., Kremer L., Lu L., Martinez A.C.,
RA Wershl B.K., Gutierrez-Ramos J.C.;
RT "Distinct expression and function of the novel mouse chemokine
RT monocyte chemotactic protein-5 in lung allergic inflammation.";
RL J. Exp. Med. 184:1939-1951(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97149438; PubMed=8996246;
RA Sarafi M.N., Garcia-Zepeda E.A., McLean J.A., Charo I.F., Luster A.D.;
RA "Murine monocyte chemoattractant protein (MCP)-5: a novel CC
RT chemokine that is a structural and functional homologue of human
RT MCP-1.";
RL J. Exp. Med. 185:99-109(1997).
RN [3]
RP SEQUENCE FROM N.A.
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RC STRAIN=B10.S/J, BALB/c, DBA/2J, NOD/LtJ, and SJL/J; TISSUE=Spleen;
RX MEDLINE=99370037; PubMed=10438970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RA Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines Scya1 (TCA-3), Scya2
RT (monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are
RT candidates for eaet, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL J. Immunol. 163:2262-2266(1999).
CC -I- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS EOSINOPHILS, MONOCYTES,
CC AND LYMPHOCYTES BUT NOT NEUTROPHILS. POTENT MONOCYTE ACTIVE
CC CHEMOKINE THAT SIGNALS THROUGH CCR2. INVOLVED IN ALLERGIC
CC INFLAMMATION AND THE HOST RESPONSE TO PATHOGENS AND MAY PLAY A
CC PIVOTAL ROLE DURING EARLY STAGES OF ALLERGIC LUNG INFLAMMATION.
CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE LYMPH NODES AND
CC THYMUS. ALSO FOUND IN THE SALIVARY GLANDS CONTAINING LYMPH NODES,
CC BREAST, HEART, LUNG, BRAIN, SMALL INTESTINE, KIDNEY AND COLON.
CC -I- INDUCTION: BY INTERFERON GAMMA AND LIPOPOLYSACCHARIDE (LPS).
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
-----
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CC EMBL; U50712; AAB50053.1; -.
CC EMBL; U6670; AAB49424.1; -.
CC EMBL; AF065934; AAF15384.1; -.
CC EMBL; AF065935; AAF15385.1; -.
CC EMBL; AF065936; AAF15386.1; -.
CC EMBL; AF065937; AAF15387.1; -.
CC EMBL; AF065938; AAF15388.1; -.
CC HSSP; P13500; 1DOL.
CC MGD; MGI:108224; Scya12.
CC InterPro: IPR000827; CC_chemkine_sml.
CC InterPro: IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CC Cytokine; Chemotaxis; Signal; Inflammatory response.
CC SIGNAL 1 22 BY SIMILARITY.
CC CHAIN 23 104 SMALL INDUCIBLE CYTOKINE A12.
CC DISULFID 33 58 BY SIMILARITY.
CC DISULFID 34 74 BY SIMILARITY.
CC VARIANT 94 104 QTFILPSCIG -> RT (IN STRAIN SJL/J).
CC SEQUENCE 104 AA; 11659 MW; 8D102F4FC3DBF CRC64;

Query Match 56.3%; Score 319.5; DB 1; Length 104;
Best Local Similarity 59.4%; Pred. No. 1.3e-28;
Matches 60; Conservative 21; Mismatches 17; Indels 3; Gaps 2;

QY 11 MKVSALLCLLMAATFSPQGLAOPDSVSIPITCCFENVINRKIPQRLSEYTRITNIQCP 70
    |||
Db 1 MKIS-TLLCLLIATITSPQVLGPDVSTPVTCCTYVKKIHYRKLKSYRRITSSQCP 59
    |||

QY 71 KEAVIFKTRGKEVCADPKERWVRDSMKHLDOIFQN--LKP 109
    :|||
Db 60 REAVIFRTILDKEICADPKERKWKVNSINHLDKTSQTFILFP 100
    :|||

RESULT 12
MCPA_BOVIN STANDARD; PRT; 99 AA.
ID MCPA_BOVIN STANDARD; PRT; 99 AA.
AC P28291;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
```


DE Monocyte chemotactic protein 1A precursor (MCP-1A) (MCP-1) (Acidic
DE seminal fluid protein).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seminal plasma;
RX MEDLINE=92096117; PubMed=1721821;
RA Wempe F., Henschen A., Scheitl K.H.;
RT "Gene expression and cDNA cloning identified a major basic protein
RT constituent of bovine seminal plasma as bovine
RT monocyte-chemoattractant protein-1 (MCP-1).";
RL DNA Cell Biol. 10:671-679(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Seminal plasma;
RX MEDLINE=92181448; PubMed=1543494;
RA Wempe F., Einspanier R., Scheitl K.H.;
RT "Characterization by cDNA cloning of the mRNA of a new growth factor
RT from bovine seminal plasma: acidic seminal fluid protein.";
RL Biochem. Biophys. Res. Commun. 183:232-237(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94338337; PubMed=8060303;
RA Wempe F., Kuhlmann J.K., Scheitl K.H.;
RT "Characterization of the bovine monocyte chemoattractant protein-1
RT gene.";
RL Biochem. Biophys. Res. Commun. 202:1272-1279(1994).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
CC NEUTROPHILS.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
DR EMBL; L32659; AAA60956.1; -.
DR EMBL; M84602; AAA30651.1; -.
DR PIR; A39296; A39296.
DR PIR; JC2336; JC2336.
DR HSSP; P13500; IDOM.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 99 MONOCYTE CHEMOTACTIC PROTEIN 1A.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
SQ SEQUENCE 99 AA; 11114 MW; 0FD79FC1AB0CBE8 CRC64;
Query Match 53.3%; Score 302; DB 1; Length 99;
Best Local Similarity 56.6%; Pred. No. 1.e-26;
Matches 56; Conservative 21; Mismatches 22; Indels 0; Gaps 0;
QY 11 MKVSAALLCLLMAATFSPQGLAQPDSVSIPTCCFENVINRKIPQRLSEYTRITNIQCP 70
DB 1 MKVSAALLCLLTVAAFTSEVLAAQPDAINSOVACCYTFSNKSISMQRMLNRYRTSSKCP 60
QY 71 KEAVIFKTRGKEVCADPKERWVRDSMKHLDOIFQNLKP 109
||||| |||:||||:||||:|:|

Db 61 KEAVIFKTLGKELCADPKQKWVQDSINYLNNKNOTPKP 99
RESULT 13
SY02_RABIT
ID SY02_RABIT STANDARD; PRT; 125 AA.
AC P28292;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN SCYA2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Spleen;
RX MEDLINE=91225489; PubMed=2026877;
RA Yoshimura T., Yuhki N.;
RT "Neutrophil attractant/activation protein-1 and monocyte
RT chemoattractant protein-1 in rabbit. cDNA cloning and their
RT expression in spleen cells.";
RL J. Immunol. 146:3483-3488(1991).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
CC NEUTROPHILS.
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
DR EMBL; M57440; AAA31386.1; -.
DR HSSP; P13500; IDOM.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response; Glycoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 125 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 125 AA; 13776 MW; 24C3A542CB6A47EE CRC64;
Query Match 52.6%; Score 298; DB 1; Length 125;
Best Local Similarity 56.1%; Pred. No. 4e-26;
Matches 55; Conservative 18; Mismatches 25; Indels 0; Gaps 0;
QY 11 MKVSAALLCLLMAATFSPQGLAQPDSVSIPTCCFENVINRKIPQRLSEYTRITNIQCP 70
DB 1 MKVSATLLCLLIIAFAFSHYLAQPDVNSPVTCYFTFNKTSIVKRLMSYRRINSTKCP 60
QY 71 KEAVIFKTRGKEVCADPKERWVRDSMKHLDOIFQNLK 108
DB 61 KEAVIFMTLAKGICADPKQKWVQDAIANLDRKMQTPK 98
||||| |||:||||:||||:|:|

```
RESULT 14
EOTA_RAT
ID EOTA_RAT STANDARD: PRT: 97 AA.
AC P97545; 008780;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Eotaxin precursor (Small inducible cytokine A11) (CCL11) (Eosinophil
DE chemotactic protein).
GN SCYA11.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98060832; PubMed=9396866;
RA Williams C.M., Newton D.J., Wilson S.A., Williams T.J., Coleman J.W.,
RA Flanagan B.F.;
RT "Conserved structure and tissue expression of rat eotaxin.";
RL Immunogenetics 47:178-180(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
MEDLINE=98120437; PubMed=9458816;
RA Ishi Y., Shirato M., Nomura A., Sakamoto T., Uchida Y., Ohtsuka M.,
RA Sagai M., Hasegawa S.;
RT "Cloning of rat eotaxin: ozone inhalation increases mRNA and protein
RT expression in lungs of brown Norway rats.";
RL Am. J. Physiol. 274:L171-L176(1998).
CC -I- FUNCTION: IN RESPONSE TO THE PRESENCE OF ALLERGENS, THIS PROTEIN
CC DIRECTLY PROMOTES THE ACCUMULATION OF EOSINOPHILS, A PROMINENT
CC FEATURE OF ALLERGIC INFLAMMATORY REACTIONS (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
DR EMBL: Y08358; CAA69645.1; -
DR EMBL: U96637; AAB65775.1; -
DR HSSP: P51671; 1EOT.
DR InterPro: IPR000827; CC_chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Eosinophil; Cytokine; Chemotaxis; Glycoprotein; Signal;
KW Inflammatory response.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 97 EOTAXIN.
FT DISULFID 32 57 BY SIMILARITY.
FT DISULFID 33 73 BY SIMILARITY.
FT CARBOHYD 94 94 O-LINKED (POTENTIAL).
SQ SEQUENCE 97 AA; 10851 MW; 77375B4A038B3F6B CRC64;

Query Match 49.9%; Score 283; DB 1; Length 97;
Best Local Similarity 55.6%; Pred. No. 1.4e-24;
Matches 55; Conservative 18; Mismatches 24; Indels 2; Gaps 1;

OY 11 MKVSALLCLLMAATFSPQGLAOPDSVIPITCCFNVINRKPIQRLLESYTRITNIQCP 70
DB 1 MQLSTALLFLLLTATFSTSQVLAHPC--SIPTSCCFTMTSKKIPMTLLKSKYKRITNNRCT 58
OY 71 KEAVIEKTRGKEVCADPKERWVDSMKHLDOIFQNLKP 109
DB 59 LKAIVEKTKLGKEICADPKKRWQDATKHLQKLOTPPKP 97
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RESULT 15
SY08_MOUSE
ID SY08_MOUSE STANDARD: PRT: 97 AA.
AC Q9Z121;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
GN SCYA8 OR MCP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustlincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -I- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES. THIS PROTEIN
CC CAN BIND HEPARIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
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CC -----
DR EMBL: AB023418; BAA75014.1; -
DR EMBL: AK007942; BAB25365.1; -
DR HSSP: P51671; 1EOT.
DR MGD: MGI:101878; SCYA8.
DR InterPro: IPR000827; CC_chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; FALSE_NEG.
KW Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 97 SMALL INDUCIBLE CYTOKINE A8.
FT DISULFID 32 57 BY SIMILARITY.
FT DISULFID 33 73 BY SIMILARITY.
SQ SEQUENCE 97 AA; 11017 MW; 65BB37222F2F98D54 CRC64;
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Query Match 49.7%; Score 282; DB 1; Length 97;
Best Local Similarity 53.5%; Pred. No. 1.8e-24;
Matches 53; Conservative 18; Mismatches 26; Indels 2; Gaps 1;

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QY 11 MKVSALLCLLLMAATFSPQGLAOPDSVSIPITCCFNVINRKIPIQRLSEYTRITNIQCP 70
    ||:|||||:| ||:| ||:|||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 1 MKIYAVLLCLLLIAPVPSPKLTGPDKA--PVTCCFHYLKLKIPLRVLKSYERINNIOCP 58

QY 71 KEAVIFKTRGKEVCADPKERWVRDSMKHLDOIQNLKP 109
    ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 59 MEAVVFQTKQGMSLCVDPTQKWVSEYMEILDQKSQILQP 97
```

Search completed: February 18, 2003, 03:03:28
Job time : 23 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 18, 2003, 02:02:16 ; Search time 81 Seconds
(without alignments)
277.273 Million cell updates/sec

Title: US-10-033-067-1
Perfect score: 567
Sequence: 1 MLKLTPLPSKMKVSAALLCL.....ERWVRDSMKHLDFQNLKP 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB	ID	Description
1	359	63.3	100	6	Q95MD5	Q95md5 bos taurus
2	321	56.6	99	6	Q9TTQ3	Q9ttq3 equus caball
3	315	55.6	100	6	Q9TTQ4	Q9ttq4 equus caball
4	313	55.2	81	6	Q9TTQ2	Q9ttq2 equus caball
5	287	50.6	97	6	Q9TTS6	Q9tts6 bos taurus
6	281	49.6	97	11	Q9Z318	Q9z318 cavia porce
7	264.5	46.6	79	4	Q95689	Q95689 homo sapien
8	259.5	45.8	75	6	Q9TTQ1	Q9ttq1 equus caball
9	259	45.7	148	11	Q9QYD7	Q9qyd7 mus musculu
10	185.5	32.7	90	13	Q9PWA6	Q9pwa6 gallus gall
11	185.5	32.7	90	13	Q910C9	Q910c9 gallus gall
12	183.5	32.4	93	4	Q96168	Q96168 homo sapien
13	179	31.6	44	6	Q9BG83	Q9bg83 pongo pygma
14	177.5	31.3	92	11	Q91ZL0	Q91z10 sigmodon hi
15	173	30.5	62	4	Q95690	Q95690 homo sapien
16	170	30.0	106	11	Q9Z292	Q9z292 cricetus

17	169.5	29.9	93	6	Q8SQA6	Q8sqab bos taurus
18	169	29.8	91	11	Q91ZL1	Q91z11 sigmodon hi
19	166.5	29.4	91	13	Q8QG57	Q8qg57 gallus gall
20	162	28.6	92	6	Q8SQ40	Q8sq40 felis silve
21	161	28.4	80	4	Q14745	Q14745 homo sapien
22	160	28.2	92	11	Q91265	Q91z65 sigmodon hi
23	156	27.5	91	13	Q8QG56	Q8qg56 gallus gall
24	154.5	27.2	93	11	Q9ERE0	Q9ere0 rattus norv
25	151	26.6	89	13	Q918E0	Q918e0 gallus gall
26	145.5	25.7	95	12	Q98158	Q98158 kaposi's sa
27	143.5	25.3	99	6	Q95N01	Q95n01 canis famil
28	133	23.5	93	11	Q9WUZ6	Q9wuz6 mus musculu
29	133	23.5	131	11	Q9R043	Q9r043 mus musculu
30	130.5	23.0	100	13	Q8QG55	Q8qg55 gallus gall
31	128	22.6	395	11	Q91V44	Q91v44 mus musculu
32	119.5	21.1	97	6	Q9BDJ2	Q9bdj2 bos taurus
33	116	20.5	97	13	Q57411	Q57411 gallus gall
34	112.5	19.8	76	11	Q9QUR9	Q9qur9 mus musculu
35	108.5	19.1	96	6	Q8SQB1	Q8sqb1 bos taurus
36	108	19.0	133	11	Q91V84	Q91v84 mus musculu
37	107.5	19.0	100	13	Q9PT05	Q9pt05 oncorhynch
38	107	18.9	92	11	Q9QZU2	Q9qzu2 mus musculu
39	105.5	18.6	76	11	Q9QUS5	Q9qus5 mus musculu
40	105	18.5	92	11	Q91ZH5	Q91zh5 rattus norv
41	104.5	18.4	101	13	Q93238	Q93238 cyprinus ca
42	103.5	18.3	100	13	Q9PT07	Q9pt07 oncorhynch
43	103.5	18.3	100	13	Q9PT06	Q9pt06 oncorhynch
44	103.5	18.3	100	13	Q9PT03	Q9pt03 oncorhynch
45	103.5	18.3	100	13	Q9W691	Q9w691 oncorhynch

ALIGNMENTS

RESULT 1

Q95MD5 PRELIMINARY; PRT; 100 AA.
ID Q95MD5
AC Q95MD5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Chemoattractant protein 2 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Werling D.;
RT "Role of chemokines in respiratory syncytial virus infection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF399641; AAK94451.1;
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 100 AA; 11001 MW; F1D308AD924FCAF6 CRC64;

Query Match 63.3%; Score 359; DB 6; Length 100;
Best Local Similarity 68.7%; Pred. No. 6.4e-34;
Matches 68; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY	11	MKVSALLCLLMATFSPQGLAQPDSVSIPTCCFNVINRKIPIQRLSEYTRITNIQCP	70
DB	2	MKVSAGITLCLLVAATFGTVLAQPDVSSTPTCCFSYINGKIPFKKLDSTRTINSQCP	61
QY	71	KEAVIFKTKRGKEVCADPKERWVRDSMKHLDFQNLKP	109
DB	62	QEAVIFKTKADRDVCAADPKQKWVOTSIRLLDQKSRTPKP	100


```
RESULT 2
O9TQ3
ID O9TQ3 PRELIMINARY; PRT; 99 AA.
AC O9TQ3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Monocyte chemoattractant protein-1 precursor.
GN MCP-1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE=21061912; PubMed=11044560;
RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
RA Collins M.E.;
RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant
RT protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
RT induction by IL-4 in dermal fibroblasts.";
RL Vet. Immunol. Immunopathol. 76:283-298(2000).
DR EMBL; AJ251189; CAB61625.1; -.
DR HSSP; P13500; 1DOM.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 99 AA; 10790 MW; BA1448F79F3423D2 CRC64;

Query Match 56.6%; Score 321; DB 6; Length 99;
Best Local Similarity 60.6%; Pred. No. 1.6e-29;
Matches 60; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

OY 11 MKVSALLCLLMAATFSPQGLAQPDSVSIPITCCFNVINRKIPQRLSYTRITNIQCP 70
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Db 1 MKVSALLCLLLTAAFSTQVLAQPDAINSPVTCCTFTGKKISSORLGSYKRVTSKCP 60

OY 71 KEAVIFKTKRGKEVCADPKERWVRDSMKHLDOIFQNLKP 109
    |||||
Db 61 KEAVIFKTI LAKEICADPEQKWQDAVKQLDKKAQTPKP 99

RESULT 3
O9TQ4
ID O9TQ4 PRELIMINARY; PRT; 100 AA.
AC O9TQ4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Eotaxin precursor.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21061912; PubMed=11044560;
RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
RA Collins M.E.;
RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant
RT protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
RT induction by IL-4 in dermal fibroblasts.";
RL Vet. Immunol. Immunopathol. 76:283-298(2000).
DR EMBL; AJ251188; CAB61624.1; -.
DR HSSP; P51671; 1EOT.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
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DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 100 AA; 11247 MW; 11F08EC00E75D50B CRC64;

Query Match 55.6%; Score 315; DB 6; Length 100;
Best Local Similarity 65.2%; Pred. No. 7.9e-29;
Matches 60; Conservative 16; Mismatches 14; Indels 2; Gaps 1;

OY 11 MKVSALLCLLMAATFSPQGLAQPDSVSIPITCCFNVINRKIPQRLSYTRITNIQCP 70
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Db 1 MKVSALLCLLLTAAFSTQVLAQP--VSISTVCCFNVASRKISFORLQSYRKITSSKCP 58

OY 71 KEAVIFKTKRGKEVCADPKERWVRDSMKHLDO 102
    ::|||
Db 59 QKAVIFKTKQAKKICADPKQKWQDAWKYLDE 90

RESULT 4
O9TQ2
ID O9TQ2 PRELIMINARY; PRT; 81 AA.
AC O9TQ2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Monocyte chemoattractant protein-2 precursor (Fragment).
GN MCP-2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE=21061912; PubMed=11044560;
RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
RA Collins M.E.;
RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant
RT protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
RT induction by IL-4 in dermal fibroblasts.";
RL Vet. Immunol. Immunopathol. 76:283-298(2000).
DR EMBL; AJ251190; CAB61626.1; -.
DR HSSP; P13500; 1DOK.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT NON_TER.
SQ SEQUENCE 81 AA; 8858 MW; A34ADE103C386B0F CRC64;

Query Match 55.2%; Score 313; DB 6; Length 81;
Best Local Similarity 72.8%; Pred. No. 1.1e-28;
Matches 59; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

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Db 1 MKVSALLCLLLTAAFSTHMLAQPDAVSIPVTCFNVKKKVPQRLSYTRITSSQCS 60

OY 71 KEAVIFKTKRGKEVCADPKER 91
    :|||
Db 61 QEAVIFKTKVDKEICADPKKK 81

RESULT 5
O9TTS6
ID O9TTS6 PRELIMINARY; PRT; 97 AA.
AC O9TTS6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
```

```

DT      01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE      Eotaxin.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Vogel B., Klinder A., Aust G.;
RT      "Molecular cloning of bovine eotaxin mRNA."
RL      Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AJ132003; CAB61617.1; -.
DR      HSSP; P51671; 1EOT.
DR      InterPro; IPR001811; Chemokine_IL8.
DR      Pfam; PF00048; IL8; 1.
DR      SMART; SM00199; SCY; 1.
SQ      SEQUENCE 97 AA; 10965 MW; 9E65F23E1DDDB743 CRC64;

```

Query Match	50.68;	Score 287;	DB 6;	length 97;
Best Local Similarity	57.18;	Pred. No. 1.3e-25;		
Matches	56;	Conservative 19;	Mismatches 21;	Indels 2;
				Gaps 1;
Qy	11	MKVSAA ¹ LC ¹ LLMAA ¹ TFSPQGLA ¹ QPD ¹ SVS ¹ IPITCC ¹ FN ¹ VR ¹ NR ¹ K ¹ IP ¹ IOR ¹ LES ¹ YTR ¹ ITN ¹ IQCP ¹ 70		
		: : :		
Db	1	MKVSAA ¹ VL ¹ CL ¹ LLTA ¹ TAT ¹ LC ¹ IO ¹ VLA ¹ Q ¹ -AS ¹ IPITCC ¹ FN ¹ MS ¹ KK ¹ IS ¹ IQ ¹ RLQ ¹ SYR ¹ K ¹ ITSS ¹ KCP ¹ 58		
Qy	71	KEAVIF ¹ K ¹ TR ¹ KG ¹ KEV ¹ CAD ¹ PK ¹ ER ¹ WR ¹ DS ¹ MK ¹ HL ¹ D ¹ IFQ ¹ N ¹ LK ¹ 108		
		: : : : : : : : : :		
Db	59	OKAVIF ¹ NT ¹ KQ ¹ NK ¹ K ¹ IC ¹ VD ¹ PE ¹ KE ¹ WQ ¹ NA ¹ ME ¹ YL ¹ NQ ¹ SQ ¹ TLK ¹ 96		

RESULT 6			
Q9Z318			
ID	Q9Z318	PRELIMINARY;	PRT; 97 AA.
AC	Q9Z318;		
DT	01-MAY-1999 (TrEMBLrel. 10, Created)		
DT	01-MAY-1999 (TrEMBLrel. 10, last sequence update)		
DT	01-MAR-2002 (TrEMBLrel. 20, last annotation update)		
DE	Monocyte chemoattractant protein-3 (MCP-3).		
OS	Cavia porcellus (Guinea pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.		
OX	NCBI_TaxID=10141;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LUNG;		
RA	Asano K., Nakamura M., Oguma T., Fukunaga K., Matsubara H.,		
RA	Ishizaka A., Yamaguchi K., Kanazawa M.;		
RT	"Differential expression of CC chemokines in guinea pig lungs during		
RT	an allergic inflammation.";		
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB014340; BAA36456.1; .		
DR	HSSP; P51671; 1EOT.		
DR	InterPro; IPR000827; CC_chemkine_sml.		
DR	InterPro; IPR001811; Chemokine_IL8.		
DR	Pfam; PF00048; IL8; 1.		
DR	SMART; SM00199; SCY; 1.		
DR	PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.		
DR	SEQUENCE 97 AA; 11159 MW; E1B9A17C165C2421 CRC64;		

Query Match	49.6%;	Score 281;	DB 11;	Length 97;
Best Local Similarity	60.9%;	Pred. No. 6.6e-25;		
Matches	56;	Conservative	18;	Mismatches 16;
			Indels	2;
			Gaps	2;

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QY      11 MKVSALLCLLLMAATFSPÖGLAQÖPDSVSIPTCCFNVINRKIPiÖRLSESYRITNIQCP 70
      1: 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      1 MÖVIAVLCLLCLLTANFESSLLAQPDGVNIS-TCYK-RSÖRIRVÖRLSESYRITSSKCP 58

QY      71 KEAVIEFTKRGKEYCADPKERWVRDSMKHLDQ 102
      : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      59 WÖAVIEFTKENREICADPKÖÖWVÖDSMKYIDK 90

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RESULT	7			
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AC	095689;			
DT	01-MAY-1999	(TREMBlrel. 10, Created)		
DT	01-MAY-1999	(TREMBlrel. 10, last sequence update)		
DT	01-MAR-2002	(TREMBlrel. 20, last annotation update)		
DE	CC-chemokine (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=FORESKIN.			
RA	Bartels J.H., Schlueter C., Richter E., Noso N., Christophers E.,			
RA	Schroeder J.M.;			
RT	"Expression of a MCP-4 like novel CC-chemokine in human dermal			
RT	fibroblasts: molecular cloning and RT-PCR analysis.";			
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; 277650; CAB01111.1; .			
DR	HSSP; P51671; LEOT.			
DR	InterPro; IPR000827; CC_chemkine.sml.			
DR	InterPro; IPR001811; Chemokine_IL8.			
DR	Pfam; PF00048; IL8; 1.			
DR	SMART; SM00199; SCY; 1.			
DR	PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.			
FT	NON_TER 1 1			
SQ	SEQUENCE 79 AA; 8987 MW; 4FCF42983D46C352 CRC64;			

Query Match	46.68;	Score 264.5;	DB 4;	Length 79;
Best Local Similarity	62.28;	Pred. No. 4.3e-23;		
Matches 46;	Conservative 17;	Mismatches 10;	Indels 1;	Gaps 1;

```

OY 27 FSPQGLAOPDVSVIPITCCFNVINKIPIORLESYTRITNIQCPEAVIEFKYRKGEVCA 86
    |:|||||{|:::| ||| :||:||||| || :||:|||||:| ||:|
Db 1 FNPQGLAOPDALNVSPSTCCFTFSSKKISLQRLKSYV-ITTSRCPQKAVIEFKTKGEICA 59

OY 87 DPKERWVRDSMKHL 100
    ||||:|:: ||||
Db 60 DPEKEWQNYMKHL 73

```

```
QY      87 DPKERWRDSMKHL 10
        |||:|:|:|
Db      60 DPKEKWQNYMKHL 73
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RESULT 8			
ID	Q9TTQ1	PRELIMINARY;	PRT; 75 AA.
AC	Q9TTQ1;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	Monocyte chemoattractant protein-4 precursor (Fragment).		
GN	MCP-4.		
OS	Equus caballus (Horse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
OX	NCBI_TaxID=9796;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=21061912; PubMed=11044560;		
RA	Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,		
RA	Collins M.E.;		
RT	"Cloning of equine chemokines eotaxin, monocyte chemoattractant		
RT	protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and		
RT	induction by IL-4 in dermal fibroblasts.";		
RL	Vet. Immunol. Immunopathol. 76:283-298(2000).		
DR	EMBL; AJ251191; CAB61627.1; -.		
DR	HSSP; P51671; LEOT.		
DR	InterPro; IPR001811; Chemokine_IL8.		
DR	Pfam; PF00048; IL8; 1.		
DR	SMART; SM00199; SCY; 1.		
KW	Signal.		


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Oy      40 IPITCFNVINRKPIQIOBLESYTRITNIQCPRKEAVIFKTKRGKEVCADPKERWVDSMKH 99
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Db       1 VPSTCFETFSKKISIQRLKSIVITTS-----SFRTKLGKEICADPKEKWQNYMKH 52

Oy      100 LDQIFQNLIK 108
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Db        53 LGRKAHTLTK 61
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Search completed: February 18, 2003, 03:05:04
Job time : 83 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 03:07:17 ; Search time 2869 Seconds

(without alignments)
8683.165 Million cell updates/sec

Title: US-10-033-067-2

Perfect score: 856
Sequence: 1 aaacctcacctctcatgct.....actaaaaaaaaaaaaaa 856

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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14: gb_vl:*
15: em_ba:*
16: em_fun:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	844.2	98.6	1368	9	HSY16645	Y16645 Homo sapien
2	841	98.2	878	9	HSMCPR02	Y10802 H.sapiens m
3	589.6	68.9	181022	9	AC011193	AC011193 Homo sapi
4	586.4	68.5	2991	9	HSMCP2	X9986 H.sapiens M
5	394.8	46.1	828	4	AF506972	AF506972 Equus cab
6	393.2	45.9	839	4	AF506972	S67954 monocyte ch
7	359.6	42.0	833	4	SSPMC2	Z48480 Sus sp. MRN
8	282.8	33.0	479	4	AF399641	AF399641 Bos tauru
9	257.6	30.1	1085	9	HSMCP3A	X72308 Homo sapien
10	256	29.9	810	9	HSMCP3	X71087 H.sapiens N
11	256	29.9	814	6	A17783	A17783 NC28 mRNA.
12	256	29.9	814	6	AR094458	AR094458 Sequence
13	244.6	28.6	767	4	ECA251189	AJ251189 Equus cab
14	238.8	27.9	813	9	HSCCHK53	Z75668 H.sapiens m
15	237	27.7	839	9	HSU46573	U46573 Human eotax
16	235.6	27.5	807	9	HUMEOTAXIN	D49372 Human mRNA
17	222	25.9	3338	4	S67956	S67956 MCP-2-monoc
18	221.4	25.9	725	9	HSMCP1	X14768 H.sapiens m
19	221.4	25.9	739	9	S71513	S71513 monocyte ch
20	221.4	25.9	741	6	E05611	E05611 cDNA encodi
21	221.4	25.9	743	9	BC009716	BC009716 Homo sapi
22	220.2	25.7	514	4	ECA251188	AJ251188 Equus cab
23	219.8	25.7	741	6	A17786	A17786 MCP-1 mRNA.
24	219.8	25.7	741	6	AR094465	AR094465 Sequence
25	219.8	25.7	741	9	HUMMCAF	M24545 Human monoc
26	218.2	25.5	630	4	CFU29653	U29653 Canis fam11
27	218	25.5	441	9	BC017850	BC017850 Homo sapi
28	216	25.2	771	4	BOVMOCHEM	M84602 Bos taurus
29	214.8	25.1	661	9	S69738	S69738 MCP-1=monoc
30	214	25.0	740	4	SSMCP1	Z48479 Sus sp. MRN
31	214	25.0	757	4	SSMCP1	X79416 S.scrofa MC
32	210.6	24.6	718	9	HUMSECPA	M28226 Human JE ge
33	205.4	24.0	399	6	BD003075	BD003075 Polynucle
34	203	23.7	825	9	HSU46767	U46767 Human monoc
35	203	23.7	829	9	BC008621	BC008621 Homo sapi
36	203	23.7	855	9	HSSCYA13	AJ001634 Homo sapi
37	203	23.7	860	9	HSU59808	U59808 Human monoc
38	201.2	23.5	317	4	ECA251190	AJ251190 Equus cab
39	200.8	23.5	300	9	AF255343	AF255343 Macaca mu
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43	194.2	22.7	330	6	E03044	E03044 cDNA encodi
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ALIGNMENTS

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DEFINITION Homo sapiens mRNA for monocyte chemotactic protein-2.
ACCESSION Y16645
VERSION Y16645.1 GI:2916795
KEYWORDS MCP-2 gene; monocyte chemotactic protein 2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 1368)
Van Coillie,E., Proost,P., Van Aelst,I., Struyf,S., Polfliet,M., De
Meester,I., Harvey,D.J., Van Damme,J. and Opendakker,G.
Functional comparison of two human monocyte chemotactic protein-2

Pred. No. is the number of results predicted by chance to have a

isoforms, role of the amino-terminal pyroglutamic acid and processing by CD26/dipeptidyl peptidase IV
Biochemistry 37 (36), 12672-12680 (1998)

JOURNAL
MEDLINE
PUBMED

98400973
9730840

REFERENCE
AUTHORS

2 (bases 1 to 1368)
Van Collille,E.

TITLE
JOURNAL

Direct Submission
Submitted (23-FEB-1998) E. Van Collille, Rega Institute for Medical Research, Minderbroedersstraat 10, 3000 Leuven, BELGIUM
Related sequences: X99886, Y10802.
Location/Qualifiers

COMMENT
FEATURES

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1.1368

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/product="unnamed"

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/gene="MCP-2"

/note="polymorphism, Lys -> Gln"

/replace="C"

BASE COUNT 457 a 292 c 243 g 376 t
ORIGIN

Query Match

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Matches 846; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Db 428 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCCFCCAAGATGAAGTTCTGCA 487

QY 61 GCGCTTCTGTGCGCTGCTCTCATGCGCAGCCACTTTCAGCCCTCAGGGACTTGCTCAGCCA 120

Db 488 GCGCTTCTGTGCGCTGCTCTCATGCGCAGCCACTTTCAGCCCTCAGGGACTTGCTCAGCCA 547

QY 121 GATTCAGTTTCCATTCACCTGCTGCTTAAAGTGATCAATAGGAAATTCCTATC 180

Db 548 GATTCAGTTTCCATTCACCTGCTGCTTAAAGTGATCAATAGGAAATTCCTATC 607

QY 181 CAGAGCGTGAGAGCTACACAGAATCACCAACATCCAATGCCCAAGGAAGCTGTGATC 240

Db 608 CAGAGCGTGAGAGCTACACAGAATCACCAACATCCAATGCCCAAGGAAGCTGTGATC 667

QY 241 TTCAGAGCCAAACGGGCAAGAGGTCTGTGTCGACCCCAAGAGAGATGGGTCAGGGAT 300

Db 668 TTCAGAGCCAAACGGGCAAGAGGTCTGTGTCGACCCCAAGAGAGATGGGTCAGGGAT 727

QY 301 TTCATGAAGCATCTGGACCAATAATTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 360

Db 728 TTCATGAAGCATCTGGACCAATAATTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 787

QY 361 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTTATTTCCCAACCTCCCCAGGTCAGT 420

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Db 788 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTTATTTTCCCAACCTCCCCAGGTCAGT 847

QY 421 GTGACATTTATTTATTTATACATCCACAAGAGATTTATTTTAATTAATTAAGCATAA 480

Db 848 GTGACATTTATTTATTTATACATCCACAAGAGATTTATTTTAATTAATTAAGCATAA 907

QY 481 TATTTCTTAAAAAGTATTTAATTAATTTAAGTTGTGATGTTTAACTCTATCTGTCA 540

Db 908 TATTTCTTAAAAAGTATTTAATTAATTTAAGTTGTGATGTTTAACTCTATCTGTCA 967

QY 541 ACATCCTAGTGAATGTAAATGCAAAATCCGTGATGTGTTTGTGTTTCCCT 600

Db 968 ACATCCTAGTGAATGTAAATGCAAAATCCGTGATGTGTTTGTGTTTCCCT 1027

QY 601 GTGAGCTCAACTAAGTTCACGGCCCAANGTCATGTCTCCCTCCACNGTNGTAGTG 660

Db 1028 GTGAGCTCAACTAAGTTCACGGCCCAANGTCATGTCTCCCTCCACNGTNGTAGTG 1087

QY 661 TTGTGGGCTCCTCCNTGGATCATCAAGGTGAACACTTAGGTATTTGGCAATCAGT 720

Db 1088 TTGTGGGCTCCTCCATGATCATCAAGGTGAACACTTTGGTATTTGGCAATCAGT 1147

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RESULT 2

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LOCUS HSMCPR02

DEFINITION H.sapiens mRNA for monocyte chemotactic protein 2.

ACCESSION Y10802

VERSION Y10802.1 GI:1924937

KEYWORDS MCP-2 gene; monocyte chemotactic protein 2.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 878)

AUTHORS Van Collille,E., Froyen,G., Nomiya,H., Miura,R., Fiten,P., Van

Aelst,I., Van Damme,J. and Oudenakker,G.

TITLE Human monocyte chemotactic protein-2: cDNA cloning and regulated

expression of mRNA in mesenchymal cells

JOURNAL Biochem. Biophys. Res. Commun. 231 (3), 726-730 (1997)

MEDLINE 97224420

PUBMED 9070881

REFERENCE 2 (bases 1 to 878)

AUTHORS Van Collille,E.

TITLE Direct Submission

JOURNAL Submitted (23-JAN-1997) E. Van Collille, Rega Institute for Medical

Research, Minderbroedersstraat 10, 3000 Leuven, BELGIUM

FEATURES

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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferrelira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
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Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Margulis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
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Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 181022)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,X., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferrelira,P., Fitzgerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Glnde,S., Gord,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
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Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Meijor,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
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O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 1, 2002 this sequence version replaced gi:7321625.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu


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----- Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L746
Center clone name: 521_P_1
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RESULT 4

HSMCP2

LOCUS HSMCP2 2991 bp DNA linear PRI 20-MAR-1997

DEFINITION H.sapiens MCP-2 gene.

ACCESSION X99886

VERSION X99886.1 GI:1905800

KEYWORDS MCP-2 gene; monocyte chemotactic protein 2; SCYA10 gene.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2991)

AUTHORS Van Coillie,E., Fiten,P., Nomiya,H., Sakaki,Y., Miura,R., Yoshie,O., Van Damme,J. and Oudenakker,G.

TITLE The human MCP-2 gene (SCYA8): cloning, sequence analysis, tissue expression, and assignment to the CC chemokine gene contig on chromosome 17q11.2

JOURNAL Genomics 40 (2), 323-331 (1997)

MEDLINE 97237052

PUBMED 9119400

REFERENCE 2 (bases 1 to 2991)

AUTHORS Oudenakker,G.M.M.

TITLE Direct Submission

JOURNAL Submitted (07-AUG-1996) G.M.M. Oudenakker, Rega Institute for Medical Research, Minderbroedersstraat 10, B 3000 Leuven, BELGIUM

FEATURES

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Best Local Similarity 97.8%; Pred. No. 3e-106;

Matches 590; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 238 ATCTTCAAGACCAACGGGGCAAGAGCTGTGCTGACCCCAAGAGAGATGGTCAGG 297

Db 1862 AGCTTCAAGACCCCAACGGGGCAAGAGCTGTGCTGACCCCAAGAGAGATGGTCAGG 1921

OY 298 GATTCATGAAGCATCTGACCAATATTTCAAAATCTGAAGCCATGAGCCTCATACAT 357

Db 1922 GATTCATGAAGCATCTGACCAATATTTCAAAATCTGAAGCCATGAGCCTCATACAT 1981

OY 358 GGACTGAGAGTCAGAGCTTGAAGAAAGCTTATTTATTTTCCCAACCTCCCCAGGTGC 417

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Db 2342 AGTGTCTCTGTAAGTCAAAATGTGCTCTTGTACTGCTGTGTTGAATGANGTTACTGT 2401

QY 778 ANATTAAGTATGGAATTTGAAAAAAATTTCAAAAAAGAAAAANATATATTAATTAA 837

Db 2402 ATATTAAGTATGGAATTTGAAAAAAATTTCAAAAAAGAAAAANATATATTAATTAA 2461

QY 838 CTA 840

Db 2462 CTA 2464

RESULT 5
AF506972

LOCUS AF506972 828 bp mRNA linear MAM 22-MAY-2002

DEFINITION Equus caballus mcp-2 mRNA, complete cds.

ACCESSION AF506972

VERSION AF506972.1 GI:21070220

KEYWORDS

SOURCE Equus caballus.

ORGANISM Equus caballus

REFERENCE 1 (bases 1 to 828)

AUTHORS Takafuji, V.A., Sharova, L.V., Crisman, M.V. and Howard, R.D.

TITLE Equus caballus monocyte chemoattractant protein-2 (mcp-2), complete cds

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 828)

AUTHORS Takafuji, V.A., Sharova, L.V., Crisman, M.V. and Howard, R.D.

TITLE Direct Submission

JOURNAL Submitted (29-APR-2002) Large Animal Clinical Sciences, Orthopedic Research Laboratory, VA-MD Regional College of Veterinary Medicine, Virginia Polytechnic Institute and State University, Duckpond Drive, Blacksburg, VA 24061, USA

FEATURES

source

1. .828

/organism="Equus caballus"

/db_xref="taxon:9796"

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46. .345

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BASE COUNT 244 a 191 c 172 g 221 t

ORIGIN

Query Match 46.1%; Score 394.8; DB 4; Length 828;
Best Local Similarity 74.3%; Pred. No. 2.8e-68;
Matches 641; Conservative 0; Mismatches 179; Indels 43; Gaps 10;

QY 1 AAACCTCACCTTCATGCTGAAGCTCACACCCCTGCCCTCCACAGATGAAGTTCTGCA 60

Db 1 AAGCCAACAACCTTCCTGGGGTGAAGTTCTCATCTCCACCTCCACATGAAGGTCCTCGCA 60

QY 61 GCGCTCTGTGCTGCTGCTCATGCGCAGCCACTTTCAGCCCTCAGGGACTGCTCAGCCA 120

Db 61 GCCCTCCTGTGCTGCTGCTCAGAGGGGTTGCTTCAGCACCCACATGTTGCTCAGCCA 120

QY 121 GATTAGTTTCCATTCCAAATCACCTGCTGCTTAAAGTGAATAGGAAATTCCTATC 180

Db 121 GATGCAAGTTTCCATCCAGTCACCTGCTGCTTGGTGTGACAAAGAAAAGTCCCATC 180

QY 181 CAGAGGCTGAGAGCTACACAAGAATCACCAACATCCAAATGCCAAGGAAGCTGTGATC 240

Db 181 CAGAGGCTGAGAGCTACACAAGAATCACCAACATCCAGCAAGCTGTGATC 240

QY 241 TTCAAGACCAACCGGGCAAGGAGGTCGTGCTGACCCCAAGGAGAGATGGGTACAGGAT 300

Db 241 TTCAAGACCAACCGGGCAAGGAGGTCGTGCTGACCCCAAGGAGAGATGGGTACAGGAT 300

QY 301 TCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGA 360

Db 301 ACCATGAAGCGCCTGGACCAAGATCCCAACCCGGAAGCCTTGAACCTTCACACCTGCGC 360

QY 361 CTGAG---AGTCAGAGCTTGAAGAAAAGCTTATTATTTT-CCCCAACCTCCCCAGGT 415

Db 361 CTGAGAGACAGTCAGAGCCTGAGGAAATCTTATTATTTTCCCCAGCCTCTCTAGAT 420

QY 416 GCAGTGACATATTTTATATTAACATCCACAAGAGATTTTAAATAATTTAAAG 475

Db 421 GCAGAGTCATATTTATTTATTTAT----TTAAAAAGAGACACTTTGGTTAATTAATTAAG 476

QY 476 CATATATTTCTTAAAAAGTATTTAATTATATTTAAGTTGTGATGTTTAACTCTAT-C 534

Db 477 CATACATTTCTTAAATAATAT----TTAATATTAAAGTTAATGATGTTTGAAGTTTGTCC 532

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Db 533 TGCCACGAATCCTCGCGAAGCACAATGCAAAAT-----TTGAGATGTGCTTTC 582

QY 595 TTTCTGTGAGCTCAACTAAGTTCAAGGCCAANGTCATT-GTTCCTCCCTCCACNGTN 653

Db 583 TTTCTGTGAGAGCTCAAGTGAAGCTCATGGAAGATGGGTTCAATCTCTCTGCTGCC 642

QY 654 CGTAGTGTGTGGGGTCTCCCTCCCTGATCATCAAGTGAACACTTAGGATATCTTTGGC 713

Db 643 TGTAAAGTTGTGAGGTTCTCCCATGATCATCGAGCAAAACACTGTAGCTTCTTGA 702

QY 714 AATCAGTGTCTCTGTAAGTCAAAATGTGCTTTGTACTGCTGTGTTGAATTTGANGTTA 773

Db 703 AATCGGTGCTCTG-AGTCAAAATGCGTGTATGAGTGTGTTGTTGAATTAATGTTA 761

QY 774 CTGTANATACTATGGAATTTGAAAAAAATTTCAAAAAAGAAAAANATATATTAATTT 833

Db 762 --TTAGATGACTATGGAATTTTCAAA-----GAAAAATATATTAATTT 804

QY 834 AAAACTAAAAAAGAAAAA 856

Db 805 TAAACTAAAAAAGAAAAA 827

RESULT 6

LOCUS S67954

DEFINITION monocyte chemoattractant protein-2 [clone c11/1] [cattle, blood

PMNs, mRNA, 839 nt].

ACCESSION S67954

VERSION S67954.1 GI:544998


```
KEYWORDS
SOURCE      Bos taurus blood PMNLs.
ORGANISM    Bos taurus
REFERENCE   1 (bases 1 to 839)
AUTHORS     Wempe,F., Hanes,J. and Scheitl,K.H.
TITLE       Cloning of the gene for bovine monocyte chemoattractant protein-2
JOURNAL     DNA Cell Biol. 13 (1), 1-8 (1994)
MEDLINE     94114084
PUBMED      8286035
REMARK      GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 142216] from the original journal article.

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BASE COUNT      251 a      185 c      162 g      241 t

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Best Local Similarity 72.6%; Pred. No. 5,8e-68;
Matches 608; Conservative 0; Mismatches 200; Indels 29; Gaps 7;

OY      2 AACCTCACCTCTCATGCTGAAGCTCACACCCCTGCCCTCCAAGATGAAGCTTCTGCAG 61
      11 1 11 11111 111111 1 1 11 111111 111111 1 1 11
Db      31 AATCGCCAACCTTCAGGCTGAAGCCCCCGTCTCACCCCTCCAACATGAAGGTCTCCGCTG 90

OY      62 CGCTCTGTGCTGCTGCTCATGCGACGCCACTTTCAGCCCTCAGGGACTTGCTCAGCCAG 121
      1 1111111 1111111 1111111 11 1 1111 11 11111111
Db      91 GGATTCTGTGTGCTGCTGCTCGTGCGAGCCACCTTCGCGCACCCAGGTGCTGCTCAGCCAG 150

OY      122 ATTCAGTTTCCATTCCAAATCACCTGCTGCTTTAACGTGATCAATAGGAAAATTCCTATCC 181
      111111111 1 111111111111111 1111111 111 1 11 11
Db      151 ATTCAGTTTCTACCCCAATCACCTGCTGCTTAGTGTGATCAATGGGAAGATCCCTCTCA 210

OY      182 AGAGCGTGGAGAGCTACACAAGAATCACCAACATCCATGTCCCAAGGAAGCTGTGATCT 241
      111 111111 1111111 1111111111 11 11111 1111111111111111
Db      211 AGAAGCTGGACAGCTACACGAGAATCACCAACAGCCAGTGTCCCAAGGAAGCTGTGATCT 270

OY      242 TCAAGACCAAAACGGGCAAGGAGGTCTGTGCTGACCCCAAGGAGAGATGGGTCAAGGATT 301
      111111111 1 1 11 111111111111111 111 11111 1 11
Db      271 TCAAGACCAAAAGCGAGAGGAGTGTGTGTGTGACCCCAAGAGAGTGGGTCCAGACTT 330

OY      302 CCATGAAGCATCTGGACCAAAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGAGAC 361
      1111 1 11 11111111 1 1 11 11111 11 1111111 1 111
Db      331 CCATGAAGCTCTCGACCAAAAGTCCCGAACACCGAAGCCTTGAACCTTCATACCTTAGAC 390

OY      362 TGAGAGTCAGAGCTTGAAGAAAGCTTATTTATTTTCCCAACCTCCCCAGGTGACGTG 421
      111111 11111 1 111 1 11 11 1111111 111111111
Db      391 TGAGAGACAGAGTCTTGAAAAATCTTATTTATTTCTTCCCAACCTTCCCCAGGTG---- 445

OY      422 TGACATTATTTTATTTATACATCCACAAGAG-ATTATTTTAAATATTTAAAGCATAA 480
      111111 111111 111 11111 11 11111 1 1 11 11 11
Db      446 ---TATTTATGTATTTATTAATGCGCAAAAGAGTTTTTTTTTTAAATATTTAAACACTT 502

OY      481 TATTTCTTAAAAAGTATTTAATTAATTAAGTTGTGATGTTTAACTCTATCTGATCAT 540
      11111111 1 11111111 11111111 11 111 11 11111 111
Db      503 AGTTTCTTAAACATATTTAATTAATTAAGTTAATGTATTTT-ACTTTATCTGCCAT 561

OY      541 ACATCCTAGTGAATGTAATAATGCAAAATCCTGGTGAATGTGTTTTTGTGTTTTGTTTCT 600
      1 111111 11111 11 1 111 111 1 11 11111
Db      562 AAATCCTAATGAATTAAGATACAACATC-----TGGTGAATGAGTTTCTT 606
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OY      601 GTGAGCTCACTAAGTTTCACGGGCCAAANGTCATTTGTTCTCCCTTACCGNGTNGTAGTG 660
      1111111 1 11111111 1 1 1 1 1111 11 1 1111
Db      607 GTGAGCTTGATTAAGTTTCACAGCAGAGATGCTGCTATT-TCCCATCTTACTGCATGTAGGA 665

OY      661 TTGTGGGGTCTCCCTCCNTGGATCATCAAGGTGAACACACTTAGGTATTTCTTGGCAATCAGT 720
      1 11 11111 11 11111 11111111 1 1 1111 1 111111
Db      666 TGTGAGAGTCTCCTTCACCTGATTAACAGAGTGAACACTTTTGGAACTTAGGAATCAGT 725

OY      721 GCTCCTGTAAGTCAATATGTGTGCTTTGTACTGCTGTGTTGAAATTTGANGTTACTGTANA 780
      1111111111 11111111 1111 1 111 1 1111 1 1111 11
Db      726 GCTCCTGTAAGT-GGATGTGTGCTATGTAGTATTGTGATGGAAGTAATGTTA--TTACA 782

OY      781 TAACTATGGAATTTGAAAAAAATTTCAAAAAAGAAAAANATATATTAATTTAAAA 837
      1 11111111111 111 1111 1 1 11 1 1 1 1 1111
Db      783 TGACTATGGAATTTCAAAATAAAAAATACATATTAATTTCAAAAAAAGAAAAA 839

RESULT 7
SSPMCP2      833 bp      mRNA      linear      MAM 23-FEB-1995
LOCUS        Sus sp. mRNA for monocyte chemoattractant protein 2.
DEFINITION   248480
ACCESSION   248480
VERSION      248480.1 GI:683718
KEYWORDS     monocyte chemoattractant protein 2.
SOURCE       Sus sp.
ORGANISM     Sus sp.
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
              Hosang,K., Knoke,I., Klaudiny,J., Wempe,F., Wuttke,W. and
              Scheitl,K.H.
              Porcine luteal cells express monocyte chemoattractant protein-2
              (MCP-2): analysis by cdna cloning and northern analysis
              Biochem. Biophys. Res. Commun. 205 (1), 148-153 (1994)

REFERENCE    2 (bases 1 to 833)
AUTHORS      Hosang,K.
TITLE        Direct Submission
JOURNAL      Submitted (23-FEB-1995) Kerstin Hosang, Abteilung fuer Molekulare
              Biologie, Max-Planck-Institut fuer Biophysikalische Chemie, Am
              Fassberg 11, Goettingen, D-37077, Germany

FEATURES
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            /protein_id="CAA88371.1"
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            /db_xref="SWISS-PROT:P49873"
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            polyA_signal 812..817
            polyA_site 833

BASE COUNT   218 a      225 c      166 g      224 t

ORIGIN
Query Match      42.0%; Score 359.6; DB 4; Length 833;
Best Local Similarity 70.3%; Pred. No. 2,6e-61;
Matches 565; Conservative 0; Mismatches 225; Indels 14; Gaps 6;

OY      18 GCTGAAGCTCACACCCCTTGCCCTCAAGATGAAGTTTCTGCAGCGCTTCTGTGCTGCT 77
      11111111 1 1 111111 111 1111 1 11111 111111 11111
Db      31 GCTGAAGCTTCCAGGCTCCCGCTCCAGCATGCAGGTCCTCCGACGCCCTTCTGTGCTGCT 90

OY      78 GCTCATGGCAGCCACTTTCAGCCCTCAGGGAGCTGCTCAGCCAGATTCAGTTTCATTC 137
      11111 1 1 1 11111 1 111 111111111111111 11111 11
Db      91 GCTCACACACCGCTGCCTTCAGACCCAGGTGCTGTGCTCAGCCAGATTCAGTCTCCATCCC 150
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OY		138	AATCACCTGCTGCTTTAAACGTGATCAATAGGAAAATTCTATCCAGAGCGCTGGAGAGCTA	197
Db		151	GATCACCCTGCTGCTTCGGTCTGCTCATGTGAAGAAGATCCCCTTCAAGAACTGGAGAGCTA	210
OY		198	CACAAGAATCACCAACATCCAATGTCCCCAAGGAAGCTTGATCTTCAAGACCMAAGCGGG	257
Db		211	CACAAGAATCACCAACAGCCAGTGTCCCCAGGAGGCTTGATCTTCAAGACCMAAGCCGA	270
OY		258	CAAGGAGTCTGTGCTGTAACCCCAAGGAGAGATGGGTCAAGGATTCCATGAAGCATCTGGA	317
Db		271	CAAGGAGTCTGTGCGCGGAGACCCCAAGCAGAGAGTGGGTCCAGAAATTCATGAAGCTCTGGA	330
OY		318	CCAAATATTTCAAATCTGAAGCCATGAGCCCTTCATACATGACTGAGAG---TCAGAG	373
Db		331	CCAGAAGTCCCAAAACCCGGAAGCCTTGAACCTTCTTACCTGGACTGGAGACCACCACAG	390
OY		374	CTTGAAGAAAAAGCTTAATTATT--TTCCCCAACCTCCCCCAGGTGCAGTGTGACATATAT	430
Db		391	TCTTAGGAAATCTTATTTATTTCTCCCTCACCTTCCCGGGTGCAGAGTGATATATAT	450
OY		431	TTTTATTATACATCCACAAGAGATTTTAAATAATTTAAAGCATATATTTCTTAA	490
Db		451	TTTA----ACGTCCCTCCAGAGGTTCTTTGTTAATTAATTAATAACACAAATGTTTGTAA	506
OY		491	AAAGTATTTAATTATATTTAAGTGTGTGATGTTTAACTATCTGTCA-TACATCCTAG	549
Db		507	ACAATATTTAATGTTATTTAAGTTATTTGATGTCCTTAACCTCATCTGCCACCTAATGAGTG	566
OY		550	TGAATGTAAATGCAAAATCCTGTGATGTGTTTTTTGTTTCTGTTCTGTGAGCTCA	609
Db		567	TAAAAAATAAAAAAAAAAACACACAGCACCTGTTGACCAAGTTTCTCTCTGTGACCTCA	626
OY		610	ACTAAGTTCACGGCCCAANGTCATGTTCTCTCCCTCCACNGTNCGTAGTGTGTGGGGT	669
Db		627	GTTAAGTTCACGGCGGAGATGGCATTTTCTCTCTCTCTCTGCTCTGTTACTGTGAAG-	685
OY		670	CCTCCNTGGATCATCAAGGTGAACACTTAGGTATCTTTGGCAATCAGTGTCTCTGTA	729
Db		686	CCTTCTGCCGATCATCGCGCTGAACACCTTGTGCTTCTTGAAGAAACGAGTCCCTTGTGA	745
OY		730	AGTCAATGTGTGCTTTGTACTGCTGTTGTTGAATGTGANTTACTGTANATACTATGG	789
Db		746	AGCCGAA-GTGTGCTGGGCGAGTATTTATTTGGAAGTGAATGTTGTACACACAGCTGTGAC	804
OY		790	AATTTGAAAAAAATTTCAAAA	813
Db		805	ATTTCAAAATTAACAGTACATACA	828
<hr/>				
RESULT 8				
AF399641			479 bp	mRNA linear MAM 23-AUG-2001
LOCUS				
DEFINITION	Bos taurus		chemoattractant protein 2 mRNA, partial cds.	
ACCESSION	AF399641			
VERSION	AF399641.1		GI:15281828	
KEYWORDS				
SOURCE	Bos taurus.			
ORGANISM	Bos taurus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
	Bovidae; Bovinae; Bos.			
REFERENCE	1 (bases 1 to 479)			
AUTHORS	Werling,D.			
TITLE	Role of chemokines in respiratory syncytial virus infection			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 479)			
AUTHORS	Werling,D.			
TITLE	Direct Submission			
JOURNAL	Submitted (11-JUL-2001) Institute of Animal Sciences, ETH Zurich,			
	Schorenstrasse 16, Schwerzenbach, ZH 8603, Switzerland			
FEATURES	location/Qualifiers			
source	1..479			

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BASE COUNT	129	a	115	c	96	g	139	t		
ORIGIN										
Query Match	33.0%	Score	282.8;	DB	4;	Length	479;			
Best Local Similarity	77.1%	Pred.	No. 4.3e-46;							
Matches	373;	Conservative	0;	Mismatches	102;	Indels	9;	Gaps	2;	
QY	43	AAGATGAAGGTTTCTGACAGCGCTTCTGTGCCCTGCTGCTCATGGCAGCCACTTTCAGCCCT	102							
Db	1	ACGATGAAGGTCCTCCGCTGGGATTTCTGTGCTGCTGCTGCTGGCAGCCACTTGGCACC	60							
QY	103	CAGGACTTGCTCAGCCAGATTCAGTTTCCATTCACATCACTGCTGCTTAAAGTGATC	162							
Db	61	CAGGTGCTCGCTCAGCCAGATTCAGTTTCTACCCCAATCACTGCTGCTTAAAGTGATC	120							
QY	163	AATAGGAATTCCTATCCAGAGGCTGGAGAGCTACACAGAAATCAACACATCCAAATGT	222							
Db	121	AATGGGAAGATCCCTTCAAGAAGCTGGACAGCTACACAGAAATCAACACAGCAAGTGT	180							
QY	223	CCCAAGGAAGCTGTGATCTTCAAGACCAACCGGGCAAGAGGCTGTGCTGACCCCAAG	282							
Db	181	CCCCAGGAAGCTGTGATCTTCAAGACCAACCGGACAGGAGTGTGCTGACCCCAAG	240							
QY	283	GAGAGATGGGTGAGGATTCATGAAGCATCTGACCAAAATTTCAAAATCTGAAGCCA	342							
Db	241	CAGAAGTGGGTCCAGACTTCATTAAGGCTCCTGGACCAAAAGTCCCGAAGCAAGGCT	300							
QY	343	TGAGCCTTCATACATGAGCTGAGAGTCAAGAGCTTGAAGAAAAGCTTATTTTCCCA	402							
Db	301	TGAACCTTCATACCTAGACTGAGAGACAGAGCTTGAAGAAATCTTATTTCTTCCA	360							
QY	403	ACCTCCCCCAGGTGACAGTGTGACATTTATTTATTAACATCCACAAGAG-ATTATTTT	461							
Db	361	ACCTTCCCGAGGTG-----TATTAATTGTATTATGAGCAAAAAGAGTTTTTT	412							
QY	462	TAAATATTTAAAGCATTAATTTCTTAAAGATATTTAATTAATTTAAGTTGTGATG	521							
Db	413	TTAATAATTTAAACACTAGTTTCTTAAACATATTTAATTAATTTAAGTTATGTTA	472							
QY	522	TTTT 525								
Db	473	TTTT 476								
RESULT 9										
LOCUS	HS MCP3A	1085 bp	mRNA	linear	PRI	25-NOV-1998				
DEFINITION	Homo sapiens mRNA for monocyte chemotactic protein-3 (MCP-3).									
ACCESSION	X72308 S57464									
VERSION	X72308.1 GI:3928270									
KEYWORDS	monocyte chemotactic protein 3.									
SOURCE	Homo sapiens.									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.									
AUTHORS	Odenakker, G., Froyen, G., Fiten, P., Proost, P. and Van Damme, J.									
TITLE	Human monocyte chemotactic protein-3 (MCP-3): molecular cloning of the cDNA and comparison with other chemokines									
JOURNAL	Biochem. Biophys. Res. Commun. 191 (2), 535-542 (1993)									
MEDLINE	93213290									
PUBMED	8461011									
REFERENCE	2 (bases 1 to 1085)									

AUTHORS	Opdenakker, G.M.			
TITLE	Direct Submission			
JOURNAL	Submitted (27-MAY-1993) G.M. Opdenakker, Rega Institute, University of Leuven, Minderbroedersstraat 10, B-3000 Leuven, BELGIUM			
REFERENCE	3 (bases 1 to 1085)			
AUTHORS	Opdenakker, G., Fiten, P., Nys, G., Froyen, G., Van Roy, N., Speleman, F., Laureys, G., and Van Damme, J.			
TITLE	The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the C-C chemokine gene cluster on chromosome 17q11.2-q12			
JOURNAL	Genomics 21 (2), 403-408 (1994)			
MEDLINE	94375065			
PUBMED	7916328			
COMMENT	On Nov 26, 1998 this sequence version replaced gi:313707.			
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BASE COUNT	314 a	214 c	229 g	328 t
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Best Local Similarity	67.9%; Pred. No. 4e-41;			
Matches 409; Conservative	0;	Mismatches 179;	Indels 14;	Gaps 3;
QY	1	AAACCTTCA	CTTCATGCTGAAGCTCACACCCCTTGCCCTCCAAAGATGAAGTTCTGCA	60
Db	284	AAACCTTCA	ATTTCTCATGTGGAAGCCCATGCCCTCACCTCCAAACATGAAGCCCTGCA	343
QY	61	GCGCTTCTG	TGCGCTGCTCATGGCAGCCACTTTCAGCCCTCAGGACTTGCTCAGCA	120
Db	344	GCACTTCTG	TGTGCTGCTCACAGCAGCTGCTTACGCCCCAGGGGCTGCTCAGCA	403
QY	121	GATTCAGTT	TCCATTCCAATCACCTGCTGCTTTAAGTGATCAATAGAAAATTCCTATC	180
Db	404	GTTGGGATT	AATACTTCACTACACTGCTGCTACAGATTTATCAATAAGAAAATCCCTAAG	463
QY	181	CAGAGGCTG	AGAGCTACACAGAATCACCAACATCCAAATGTCCCAAGGAAGCTGTGATC	240
Db	464	CAGAGGCTG	AGAGCTACACAGAAGCAACCAAGTACCACTGTCCCGGGAAGCTGTATC	523
QY	241	TTCAAGACC	AAACGGGCAAGGAGGTCTGTGCTGAGCCCAAGGAGAGATGGGTACAGGAT	300
Db	524	TTCAAGACC	AAACGGGCAAGGAGATCTGTGCTGAGCCCAACAGAGAGTGGGTCCAGGAC	583
QY	301	TCCATGAAG	CATCTGAGCAACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGA	360
Db	584	TTTATGAAG	CACCTGAGCAAGAAAACCAAACTCCAAAGCTTTGAACATTCATGACTGAA	643
QY	361	CTGAG---	AGTCAGAGCTTGAGAAAAGCTTTATTTTCCCAACCTCCCCCAAGGTG	416
Db	644	CTGAAAACA	AGCCATGACTTGAGAAAACCAATATTTGTAATACCCCTGTCCTTCTCAGAGT	703
QY	417	CAGTGTGAC	ATTATTTATTAACATCCACAAAGA-GATTATTTTAAATTAATTTAAAG	475

Db	704	GGTCTGAGATTATTTAACTTAATTTCTAAGGAATATGAGCTTTATGTAAATGTGAAT	763
OY	476	CATAATATTTCTTAAAGATATTTAATATATATTTAACTTGTGATGTTTAACTCTATCT	535
Db	764	CATGGTTTCTTCTAGTATTTAA-----AAGTATTATATATTTAAATTTAATCT	814
OY	536	GTCATACATCCTAGTGAATGTAAATGC AAAATCCTGATGATGTTTGTGTTTGT	595
Db	815	TCCATGGAATTTGGTGGCTTTTGAACATAAGCCTTGATGTATATGTCATCTCAGTCT	874
OY	596	TT 597	
Db	875	GT 876	
RESULT	10		
HSMCP3			
LOCUS	HSMCP3	810 bp	mRNA linear PRI 07-AUG-1993
DEFINITION	H.sapiens NC28 mRNA for monocyte chemoattractant protein (MCP-3).		
ACCESSION	X71087		
VERSION	X71087.1	GI:288396	
KEYWORDS	cytokine; monocyte-chemoattractant protein.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 810)		
	Minty,A., Chalon,P., Guillemot,J.C., Kaghad,M., Liauzun,P., Magazin,M., Miloux,B., Minty,C., Ramond,P., Vita,N., Lupker,J., Shire,D., Ferrara,P. and Caput,D.		
TITLE	Molecular cloning of the MCP-3 chemokine gene and regulation of its expression		
JOURNAL	Eur. Cytokine Netw. 4 (2), 99-110 (1993)		
MEDLINE	93305913		
PUBMED	8318676		
REFERENCE	2 (bases 1 to 810)		
AUTHORS	Minty,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-MAR-1993) A. Minty, Sanofi Elf Bio Recherches, Labege BP 137, 31676 Labege Cedex, FRANCE		
FEATURES	Location/Qualifiers		
source	1..810		
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CDS	41..370		
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		/note="ATTTA motif"	
polyA_signal		787.792	
BASE COUNT		248 a 169 c 155 g 238 t	
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Query Match		29.9%; Score 256; DB 9; Length 810;	
Best Local Similarity		67.8%; Pred. No. 8.4e-41;	
Matches 408; Conservative		0; Mismatches 180; Indels 14; Gaps 3;	
QY	1	AAACCTTCACCTCTCAGCTGAGCTCACACCCCTTGCCCTCCAAAGATGAAGTTCTGCA	60
DB	26	AAACCTCCAAATCTCAGTGTGGAAGCCCATGCCCTCACCCCTCAACATGAAGCCCTGCA	85
QY	61	GCGCTTCTGTGCTGCTGCTCATGGCAGCCACTTCAGCCCTCAGGGACTTGCTCAGCCA	120
DB	86	GCACTTCTGTGCTGCTGCTCAGCAGCAGCTGCTTCAAGCCCAAGGGCTGCTCAGCCA	145
QY	121	GATTCAGTTTCCATTCCAATCACCTGCTGCTTTAACGTGATCAATAGAAATTCCTATC	180
DB	146	GTTGGATTAACTACTCAACTGCTGCTGCTACAGATTATCAATAAGAAATCCCTAAG	205
QY	181	CAGAGCTGAGAGCTPACAGAAATCACCAACATCCAAATGTCCCAAGGAAGCTGTATC	240
DB	206	CAGAGGCTGAGAGCTACAGAAAGAACACAGTAGCCACTGTCCCCGGAAGCTGTATC	265
QY	241	TTCAAGACCAACGGGGCAGGAGTCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT	300
DB	266	TTCAAGACCAAACTGGACAGAGATCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT	325
QY	301	TCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCATGAGCCTTCATACATGGA	360
DB	326	TTTATGAAGCACCCTGGACAAAGAAACCCTCAAGCTTTGAACATTCATGACTGAA	385
QY	361	CTGA---GAGTCAGAGCTGGAAGAAAGCTTATTTATTTCCCAACCTCCCCAGGTG	416
DB	386	CTAAAAACAAGCCATGACTGAGAAACAATATTTGTAACCTGTCCTTCTCAGAGT	445
QY	417	CAGTGTGACATTTATTTATTAACATCCACAAGA-GATTATTTTAAATAATTTAAG	475
DB	446	GTTCTGAGATTATTTAATCTAATTTCTAAGGAATATGAGCTTTATGTAATAATGTGAAT	505
QY	476	CATAATATTTCTTAAAAAGTATTTAATTAATTTAAGTGTGATGTTTAACTCTATCT	535
DB	506	CATGGTTTCTTCTAGTAGATTTTAA-----AAGTTATTAATATTTTAAATTTAATCT	556
QY	536	GTCATACATCCTAGTGAATGTAATAATGCCAAATCCGTGATGCTTTTGTGTTTGTGTT	595
DB	557	TCCATGGAATTTGGTGGTTTGAACATAAAGCCTTGATGTATATGTCATCTCAGTGT	616
QY	596	TT 597	
DB	617	GT 618	
RESULT 11			
LOCUS A17783 814 bp mRNA linear PAT 30-SEP-1994			
DEFINITION NC28 mRNA.			
ACCESSION A17783			
VERSION A17783.1 GI:641142			
KEYWORDS			
SOURCE unidentified.			
ORGANISM unidentified			

REFERENCE	1 (bases 1 to 814)	unclassified.
AUTHORS	Caput,D., Ferrara,P., Miloux,B., Minty,A. and Vita,N.	
TITLE	Protein with cytokine activity, recombinant DNA, expression vector and hosts for obtaining it	
JOURNAL	Patent: EP 0488900-A 22 03-JUN-1992;	
	ELF SANOFI	
FEATURES	Location/Qualifiers	
source	1. 814	
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	CYRFINKRIPKORLESYRRTTSSHCPRFAVIEFKTKLDKEICADPQKWODFMKHLDK	
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BASE COUNT	252 a 169 c 155 g 238 t	
ORIGIN		
Query Match	29.9%; Score 256; DB 6; Length 814;	
Best Local Similarity	67.8%; Pred. No. 8.4e-41;	
Matches	408; Conservative 0; Mismatches 180; Indels 14; Gaps 3;	
QY	1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAAGATGAAGGTTCTGCA	60
Db		26
	AAACCTCCATTTCTCATGTGGAAGAGCCCATGCCCTCACCTCCAACATGAAGCCCTGCA	85
QY	61 GCGCTTCTGTGCGCTGCTCATGGCAGCCACTTTCAGCCCTCAGGACTTGCTCAGCCA	120
Db		86
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QY	121 GATTCAGTTTCCATTTCCAATCACCTGCTGCTTTAACGTGATCAATAGGAATTCCTATC	180
Db		146
	GTTGGGATTATACTTCAACTACCTGCTGCTACAGATTATCAATAAGAAATCCCTAAG	205
QY	181 CAGAGGCTGAGAGCTACACAAGAAATCACCAACATCCAATGTCCCAAGGAAGCTGTATC	240
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	CAGAGGCTGAGAGCTACAGAAGAGCACCACAGTAGCCACTGTCCCGGAAGCTGTAATC	265
QY	241 TTCAAGACCAACGGGGCAAGGAGTCTGTGCTGAGCCCAAGAGAGATGGTTCAGGGAT	300
Db		266
	TTCAAGACCAAACTGAGACAAGAGATCTGTGCTGAGCCCAACACAGAAGTGGTCCAGGAC	325
QY	301 TCCATGAAGCATCTGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGA	360
Db		326
	TTTATGAAGCACCCTGGACAGAAAACCCAACTCCAAGCTTGAACATTCATGACTGAA	385
QY	361 CTGA----GAGTCAGAGCTTGAAGAAAAGCTTATTTTCCCCCAACCTCCCCCAGGTG	416
Db		386
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QY	417 CAGTGTGACATTTATTTATTAACATCCACAAAGA-GATTATTTTAAATAATTTAAAG	475
Db		446
	GTTTCTGAGATTATTTAATCTAATTTCTAAGGAATAGAGCTTTATGTAATAATGCAAT	505
QY	476 CATAATATTTCTTAAAAAGATTTTAATTATATTAAAGTGTGATGTTTAACTCTATCT	535
Db		506
	CATGGTTTTTCTTAGTAGATTTTAA-----AAGTTATTAATATTTTAAATTAATCT	556
QY	536 GTCATACATCCTAGTGAATGTAATAATGCAAAATCCTGGTGATGTTTTTTGTTTTGTT	595
Db		557
	TCCATGGAATTTTGGTGGGTTTGAACATAAAGCCTTGATGTATATGTCATCTCAGTCT	616
QY	596 TT 597	
Db	617 GT 618	

RESULT 12
LOCUS AR094458 814 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 15 from patent US 6001649.
ACCESSION AR094458
VERSION AR094458.1 GI:10021399
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 814)
AUTHORS Caput,D., Ferrara,P., Miloux,B., Minty,A. and Vita,N.
TITLE Chemokine NC28 (monocyte chemoattractant protein-3, MCP-3) polypeptides
JOURNAL Patent: US 6001649-A 15 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..814
BASE COUNT 252 a 169 c 155 g 238 t
ORIGIN

Query Match 29.9%; Score 256; DB 6; Length 814;
Best Local Similarity 67.8%; Pred. No. 8.4e-41;
Matches 408; Conservative 0; Mismatches 180; Indels 14; Gaps 3;

QY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAGATGAAGTTTCTGCA 60
Db 26 AAACCTCCAAATTTCTCATGTGGAAAGCCCATGCCCTCACCCCTCCACATGAAGCCTCTGCA 85
QY 61 GCGCTTCTGCTGCTGCTGCTCATGCGCAGCCACTTTAGCCCTCAGGAGCTTGTCTAGCCA 120
Db 86 GCACCTCTGCTGCTGCTGCTGCTCAGCAGCAGCTGCTTTCAGCCCCCAGGGGCTGCTCAGCCA 145
QY 121 GATTCAAGTTTCCATTTCCATCACCCTGCTGCTTTAAGTGATCAATAGAAATTCCTATC 180
Db 146 GTTGGATTAAATACTTCAACTACCTGCTGCTACAGATTATCAATAAGAAATCCCTAAG 205
QY 181 CAGAGGCTGAGAGAGCTACACAGAATCACCAACATCCATGTCCCAAGAGCTGTGATC 240
Db 206 CAGAGGCTGAGAGAGCTACAGAAGACCACAGTACCCTGCTCCCGGGAAGCTGTAATC 265
QY 241 TTCAAGACCAACAGGGGCAAGAGGCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT 300
Db 266 TTCAAGACCAACTGGACAGAAGAGATCTGTGCTGACCCCAACAGAAGTGGGTCCAGGAC 325
QY 301 TCCATGAGCATCTGGACCAATATTTCAAAAATCTGAAGCCATGAGCCTTCATACATGGA 360
Db 326 TTTATGAAGCACTGGACAAAGAAACCAACTCCAAAGCTTTGAACATTCATGACTGAA 385
QY 361 CTGA---GAGTCAGAGCTTGAAGAAAGCTTATTTTCCCAACCTCCCCAGGTG 416
Db 386 CTAAAAACAAGCCATGACTTGAGAAACAATAATTGTATACCTGCTCCTTCTCAGAGT 445
QY 417 CAGTGTGACATTTATTTATTAACATCCACAAGA-GATTATTTTAAATAATTTAAAG 475
Db 446 GGTCTGAGATTTATTTAATCTAATCTAAGGAATATGAGCTTTATGTAATATGTAAT 505
QY 476 CATAATATTTCTTAAAGATATTTAATTTAAGTGTGTGATGTTTAACTCTATCT 535
Db 506 CATGGTTTTCTTAGTAGATTTAA-----AAGTTATTAATTTAATTTAATCT 556
QY 536 GTCAATACATCTAGTGAATGTAATAATGCAAAATCCTGGTATGTTTGTGTTTGT 595
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QY 596 TT 597
Db 617 GT 618

RESULT 13
LOCUS ECA251189 767 bp mRNA linear MAM 09-NOV-2000

DEFINITION Equus caballus mRNA for monocyte chemoattractant protein-1 (mcp-1 gene).
ACCESSION AJ251189
VERSION AJ251189.1 GI:6468532
KEYWORDS MCP-1 gene; monocyte chemoattractant protein-1.
SOURCE horse.
ORGANISM Equus caballus
REFERENCE 1 (bases 1 to 767)
AUTHORS Benarafa,C., Cunningham,F.M., Hamblin,A.S., Horohov,D.W. and Collins,M.E.
TITLE Cloning of equine chemokines eotaxin, monocyte chemoattractant protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and induction by IL-4 in dermal fibroblasts
JOURNAL Vet. Immunol. Immunopathol. 76 (3-4), 283-298 (2000)
MEDLINE 21061912
PUBMED 11044560
REFERENCE 2 (bases 1 to 767)
AUTHORS Benarafa,C.
TITLE Direct Submission
JOURNAL Submitted (22-NOV-1999) Benarafa C., Department of Pathology and Infectious Diseases, The Royal Veterinary College, Hawkshead Lane, North Mymms, Hatfield, Hertfordshire AL9 7TA, United Kingdom
FEATURES Location/Qualifiers
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BASE COUNT 232 a 176 c 149 g 210 t
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Query Match 28.6%; Score 244.6; DB 4; Length 767;
Best Local Similarity 65.5%; Pred. No. 1.5e-38;
Matches 395; Conservative 0; Mismatches 194; Indels 14; Gaps 2;

QY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAGATGAAGTTTCTGCA 60
Db 10 AAACCAACAACCTCAGGCCGAGCTCCCATCTTACCCTCCAGCATGAAGTCTCTGCA 69
QY 61 GCGCTTCTGTGCTGCTGCTGCTGCTGCTTACGCTTACGAGGAGCTGCTCAGCCA 120
Db 70 GCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTTACGCTTACGAGGAGCTGCTCAGCCA 129
QY 121 GATTCAGTTTCCATTTCCATGACCTGCTGCTTAAAGTGTATCAATAGGAAATTCCTATC 180
Db 130 GATGCAATTAATTTCTCAGTCACTGCTGCTATACATTCACCGGTAAAGATCTCATCT 189
QY 181 CAGAGGCTGAGAGCTACACAGAATCACCAACATCCAAATGTCCCAAGAGCTGTGATC 240
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Db	310	GCTGTGAAGCAGCTGGACAGAAAGCCCAAACTCCAAAGCCTTGAACACCTACTCCAAA	369
QY	360	ACTGAGAGTCAGAGCTTGAAGAAAAGCTTATTTATTTCCCAACCTCCCGCAGTGCAG	419
Db	370	GCCAAGAATCTGAAGCTAATTTATTTGCTCTTAGCATTTCCCTAAATGCCCTG-----	423
QY	420	TGTGACATTATTTATTTAACAATCCACAAGAGATTTATTTAATAATTTAAGCATTA	479
Db	424	-----ATATTATTTATTTATAGTTTCAAGAGATGCAACTTTGTTTATTGACATGAAA	476
QY	480	ATATTCTTAAAAAGTATTTAATTTATTTAAGTTGTTGATGTTTAACTCTATCTGTCA	539
Db	477	CTTGATGCTTAAGTAGCGTTAATCTTATTTAAGTTATGATGTTTAAAGTTATCTTCCA	536
QY	540	TACATCCTAGTGAATGTAAATGCAGAAATCCCTGGATGCTGTTTGTGTTTGTGTTCC	599
Db	537	CGAATACTAGTGTCTGTGAGATATGAGACTTGAGCAAACTGCTTCTCTGTGAACCC	596
QY	600	TGT	602
Db	597	AGT	599
RESULT 14			
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LOCUS	HSCCCHK53	813 bp	mRNA linear PRI 10-SEP-1996
DEFINITION	H.sapiens mRNA for CC-chemokine, eotaxin variant (clone 53).		
ACCESSION	Z75668		
VERSION	Z75668.1 GI:1531982		
KEYWORDS	CC-chemokine.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 813)		
AUTHORS	Bartels,J., Schluter,C., Richter,E., Noso,N., Kulke,R.,		
TITLE	Human dermal fibroblasts express eotaxin: molecular cloning, mRNA expression, and identification of eotaxin sequence variants		
JOURNAL	Biochem. Biophys. Res. Commun. 225 (3), 1045-1051 (1996)		
MEDLINE	96374440		
PUBMED	8780731		
REFERENCE	2 (bases 1 to 813)		
AUTHORS	Bartels,J.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-JUL-1996) Bartels J. H.,		
	Christian-Albrechts-Universitaet zu Kiel, Dermatologie/Hautklinik,		
	Mol.Biol.Lab.609, Schittenhelmstr. 7, Kiel, Schleswig-Holstein,		
	Germany, D-24105		
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CDS			
mRNA			

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                  347. .>813
                  508. .517
                  /note="Two AUUUA pentanucleotides arranged in tandem
                  within a U-rich region typical for short lived cytokine
                  mRNAs"

polyA_signal      734. .739
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misc_RNA          782. .786
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                  cytokine mRNAs"

BASE COUNT       251 a      197 c      143 g      222 t
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Query Match      27.9%; Score 238.8; DB 9; Length 813;
Best Local Similarity 64.6%; Pred. No. 2.1e-37;
Matches 452; Conservative 0; Mismatches 231; Indels 17; Gaps 6;

QY      1 AAACCTTCACCTCTCAGCTGAAGCTCACACCCCTTGCCCTCCAGAATGAGGTTCTGCA 60
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Db      11 AAACCTCCACTCTCTCAGGCCAAAGCTCACACCTTCAGCCTCCAAACATGAAGGCTCCGCA 70

QY      61 GCGCTTCTGTGCCCTGCTGCTCATGGCAGCCACTTTCAGCCCTCAGGACTTGCTCAGCCA 120
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      71 GCACTTCTGTGGCTGCTGCTCATAGCAGCTGCTTCAGCCCCAGGGGCTCAGTGCGCA 130

QY      121 GATTCAAGTTCCATTCCAAATCACCTGCTGCTTTAACGTGATCAATAGAAATTCCTATC 180
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Db      131 GCTTCTG-----TCCCAACCACTGCTGCTTTAACCTGGCCCAATAGGAAGATACCCCTT 184

QY      181 CAGAGGCTGAGAGCTACACAGAATCACCAACATCCAAATGTCCCAAGGAAGCTGTGATC 240
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      185 CAGCGACTAGAGAGCTACAGAGAAATCACAGGTGGCAAAATGTCCCCAGAAAGCTGTGATC 244

QY      241 TTCAAGACCAAAAGGGGCAAGAGAGTCTGTGCTGACCCCAAGAGAGATGGGTACAGGAT 300
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      245 TTCAAGACCAAACTGGCCCAAGATATCTGTGCCGACCCCAAGAGAGGTGGGTACAGAT 304

QY      301 TCCATGAAGCATCTGGACCAATAATTTCAAAATCTGAAGCCATGAGCCTTCATACA--TG 358
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      305 TCCATGAAGTATCTGGACCAAAAATCTCCAACCTCCAAGCCATAAATATCACCATTTT 364

QY      359 GACTGAGAGTCAGAGCTTGAAGAAAAGCTTATTATTTCCTCCCAACCTCCCCAGGTGCA 418
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      365 GAAACCAAAACAGAGCCTGAGCTGTGCTTAATTGTTTC-----CCTTCTTACAATGCA 419

QY      419 GTGTGACATATTATTTATTAATCATCCACAAGA-GATTATTTTAAATAATTAAAGCA 477
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Db      420 TTCTGAGGTAACCTCATTAATCAGTCCCAAGGCGATGGGTTTATTAATATATATATATA 479

QY      478 TAATATTTCTTAAAAAGTATTAATTAATTTAAGTGTGATCTTTTAAGTCTTAACTC-TATCTG 536
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      480 TATTTTTTTAAAAAAGTATTTGCAATTTAATTTATGAGGCTTTAAAACTATATCCT 539

QY      537 TCATACATCTAGTGAATGTAATGCAAAATCTGGTGATG--TGTTTGTGTTTGT 594
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      540 CCATGAATATCAGTTACTTTTAAACTGTAAAGCTTTGTGACAGATCTTTAACCCCTGGGA 599

QY      595 TTTCCTGTGAGCTCAACTAAGTTACAGGCCAAANGTCATGTGTCTCCCTACCGTNG 654
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QY      655 GTAGTGTGTGGGCTCCNTGATCATCAAGTGAAA 694
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Db      660 GGAATCTTTAAAGTCTCGCAAAAGATGATCATGATGAAA 699

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RESULT 15
HSU46573
LOCUS HSU46573 839 bp mRNA linear PRI 03-MAY-1996
DEFINITION Human eotaxin precursor mRNA, complete cds.
ACCESSION U46573
VERSION U46573.1 GI:1280140
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 839)
Garcia-Zepeda, E.A., Rothenberg, M.E., Ownbey, R.T., Celestin, J.,
Ledger, P. and Luster, A.D.
TITLE Human eotaxin is a specific chemoattractant for eosinophil cells
and provides a new mechanism to explain tissue eosinophilia
JOURNAL Nat. Med. 2 (4), 449-456 (1996)
MEDLINE 96181758
PUBMED 8597956
REFERENCE
AUTHORS 2 (bases 1 to 839)
Garcia-Zepeda, E.A., Sarafi, M.N. and Luster, A.D.
TITLE Direct Submission
JOURNAL Submitted (18-JAN-1996) Eduardo A. Garcia-Zepeda, Infectious
Disease Unit, Department of Medicine, Massachusetts General
Hospital-East, 13th St., Charlestown, MA 02129, USA
FEATURES
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54. .347
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BASE COUNT 235 a 204 c 159 g 241 t
ORIGIN
Query Match 27.7%; Score 237; DB 9; Length 839;
Best Local Similarity 68.6%; Pred. No. 4.9e-37;
Matches 404; Conservative 0; Mismatches 170; Indels 15; Gaps 5;

Db 243 TTCAAGACCAAACTGGCCCAAGGATATCTGTGCCGACCCCAAGAAAGTGGTGACGAT 302
QY 301 TCCATGAAGCATCTGGACCAATAATTTCAAAATCTGAAGCCATGAGCCTTCATACATG-- 358
Db 303 TCCATGAAGTATCTGGACCAAAATATCTCCAACTCCAAAGCCATAAATATCACCATTATT 362
QY 359 GACTGAGAGTCAGAGCTTGAAGAAAGCTTATTATTTCCTCCCAACCTCCCCAGGTGCA 418
Db 363 GAAACCAAAACAGAGCCCTGAGTGTGCCCTAATTGTGTTTC-----CCTCTTACAATGCA 417
QY 419 GTGTGACATATTATTATTATAACATCCACAAAGA-GATTATTTTTAATAATTAAAGCA 477
Db 418 TTCTGAGGTAACCTCATTTATCAGTCCAAAGGCGATGGTTTATATATATATATATATA 477
QY 478 TAATATTTCTTAAAAAGTATTATATATATTAAAGTTGTGATGTTTAACTC-TATCTG 536
Db 478 TATTTTTTTAAAAAAAACGTATTCATTTAATTGAGGCTTTAAACTATATCC 537
QY 537 TCATACATCCTAGTGAATGTAATAATGCCAAATCCTGTGATGTGTTT 585
Db 538 CCATGAATATCAGTTATTTTAAACTGTAAAGCTTTGTGCAGATTCTTT 586

Search completed: February 18, 2003, 04:08:41
Job time : 2945 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 03:06:02 ; Search time 262 Seconds
(without alignments)
7357.674 Million cell updates/sec

Title: US-10-033-067-2
Perfect score: 856
Sequence: 1 aaacctcacctctcatgct.....actaaaaaaaaaaaaa 856

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002: *
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2: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA1981.DAT: *
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23: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
24: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	849	99.2	856	19	AAV09218 Human MC proprotei
2	841	98.2	2738	21	AAA74886 Human chemokine MC
3	588.8	68.8	9475	24	ABK70707 Reference sequence
4	378.4	44.2	411	18	AA791023 Human beta-chemoki
5	257.6	30.1	1085	21	AAF21017 Human low adenosin
6	257.6	30.1	1085	21	AAF21018 Human low adenosin
7	257.6	30.1	1085	21	AAA74887 Human chemokine MC
8	257.6	30.1	1085	21	AAA34895 Human adenosine re
9	257.6	30.1	1085	21	AAA34896 Human adenosine re

10	257.6	30.1	1085	24	ABK84649 Human CDNA differe
11	257.6	30.1	1706	22	AA544714 Full-length polynu
12	257.6	30.1	5865	21	AAF21020 Human low adenosin
13	257.6	30.1	5865	21	AAA34898 Human adenosine re
14	256	29.9	810	21	AAF21016 Human low adenosin
15	256	29.9	810	21	AAA34894 Human adenosine re
16	256	29.9	814	13	AAQ25259 Chemottractant b
17	254.4	29.7	810	16	AAQ85371 Chemottractant pr
18	250	29.2	290	21	AAA43840 Human secreted exp
19	244	28.5	256	19	AAV09221 Human MC proprotei
20	237	27.7	839	21	AAAF74879 Human chemokine co
21	235.6	27.5	807	21	AAF20924 Human ectaxin poly
22	235.6	27.5	807	21	AAA34802 Human adenosine re
23	235.6	27.5	859	18	AAT62944 Human eosinocyte C
24	235.6	27.5	3756	21	AAF20927 Human ectaxin poly
25	235.6	27.5	3756	21	AAA34805 Human adenosine re
26	235.6	27.5	209273	21	AAF21437 Human factor-relat
27	233.2	27.2	605	24	ABN86336 Human eotaxin enco
28	222.6	26.0	1712	19	AAV34249 Human secreted pro
29	222.6	26.0	1822	19	AAV34248 Human secreted pro
30	221.4	25.9	725	16	AAQ85370 Chemottractant pr
31	221.4	25.9	725	20	AAAX80631 Monocyte chemoaatr
32	221.4	25.9	802	20	AA233515 Human prostate can
33	219.8	25.7	741	13	AAQ30748 pHMCf7. Synthetic
34	219.8	25.7	741	21	AAAF21021 Human low adenosin
35	219.8	25.7	741	21	AAA34899 Human adenosine re
36	218.8	25.6	738	10	AAN91337 DNA which encodes
37	218.2	25.5	739	19	AAV10341 CDNA encoding a ma
38	218	25.5	787	13	AAQ27946 Sequence encoding
39	216.2	25.3	2281	22	AAI92896 Human polynucleoti
40	214.8	25.1	661	21	AAA74882 Human chemokine co
41	213	24.9	236	19	AAV09219 Human MC proprotei
42	209.6	24.5	386	21	AAA43570 Human secreted exp
43	208.4	24.3	330	24	AAL38341 Coding sequence of
44	207.8	24.3	436	24	ABQ57866 Human colon cancer
45	206.6	24.1	382	20	AAV86197 EST clone M100. H

ALIGNMENTS

RESULT 1						
AAV09218						
ID	AAV09218	standard;	DNA;	856 BP.		
XX						
AC	AAV09218;					
XX						
DT	09-JUN-1998	(first entry)				
XX						
DE	Human MC proprotein cDNA.					
XX						
KW	Human monocyte chemotactic proprotein; MCCP; Incyte clone; allergy;					
KW	macrophage; diagnostic assay; body fluid; lung; biopsy;					
KW	autoimmune disease; AIDS; asthma; rheumatoid arthritis; NIDDM;					
KW	breast cancer; bladder; ss.					
XX						
OS	Homo sapiens.					
XX						
FH						
FT	Key	Location/Qualifiers				
FT	CDS	16..345				
FT	/*tag= a					
FT	/product= "monocyte chemotactic proprotein"					
XX						
PN	WO9802459-A1.					
XX						
PD	22-JAN-1998.					
XX						
PF	15-JUL-1997; 97WO-US12349.					
XX						
PR	15-JUL-1996; 96US-0683655.					
XX						
PA	(INCY-) INCYTE PHARM INC.					
XX						

PI Au-Young J, Coleman R, Hillman JL;
XX WPI; 1998-110529/10.
DR P-PSDB; AAM42072.
XX
PT New human monocyte chemotactic proprotein - has homology to CC
PT chemokine(s) useful for identifying agent for treating auto-immune
PT diseases or allergic responses
XX
PS Claim 4; Page 39; 53pp; English.
XX
CC The human monocyte chemotactic proprotein cDNA sequence given was
CC first identified in Incyte clone 965517 from a breast cDNA library.
CC Antisense nucleotides can be used to control human MCPP expression
CC especially where it may lead to inappropriate monocyte or macrophage
CC activity causing damage associated with allergic responses to organs
CC such as the lungs. Antisense nucleotides and MCPP cDNA may be used
CC in diagnostic assays of body fluids or biopsied tissues to detect
CC expression levels of MCPP. MCPP cDNA may also be useful for
CC treatment of disorders such as asthma, rheumatoid arthritis, NIDDM
CC or cancer of the breast or bladder. Human MCPP protein can be used to
CC identify agonists, antagonists or inhibitors to modulate the activity of
CC MCPP in allergic responses or autoimmune diseases such as AIDS.
XX
SQ Sequence 856 BP; 261 A; 175 C; 157 G; 256 T; 7 other;

Query Match 99.2%; Score 849; DB 19; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.4e-161;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCTCCAAGATGAAGTTCTGCA 60
DB 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCTCCAAGATGAAGTTCTGCA 60

QY 61 GCGCTTCTGTGCTGCTGCTCATGCGAGCCACCTTTCAGCCCTCAGGACTGCTGACCCA 120
DB 61 GCGCTTCTGTGCTGCTGCTCATGCGAGCCACCTTTCAGCCCTCAGGACTGCTGACCCA 120

QY 121 GATTCAGTTTCCATGCCATTCACCTGCTGCTTAACTGATCATATAGGAAATPCTATC 180
DB 121 GATTCAGTTTCCATGCCATTCACCTGCTGCTTAACTGATCATATAGGAAATPCTATC 180

QY 181 CAGAGGCTGAGAGCTACACAGAATCACCAACATCCAAATGTCCCAAGAGAGCTGTGATC 240
DB 181 CAGAGGCTGAGAGCTACACAGAATCACCAACATCCAAATGTCCCAAGAGAGCTGTGATC 240

QY 241 TTCAGAGCCAAACGGGCAAGAGGTCTGTGCTGACCCCAAGAGAGATGGGTACGGAT 300
DB 241 TTCAGAGCCAAACGGGCAAGAGGTCTGTGCTGACCCCAAGAGAGATGGGTACGGAT 300

QY 301 TCCATGAAGCATCTGGACCAAAATATTTCAAATCTGAAGCCATGAGCCTTCATACATGA 360
DB 301 TCCATGAAGCATCTGGACCAAAATATTTCAAATCTGAAGCCATGAGCCTTCATACATGA 360

QY 361 CTGAGAGTCAGAGCTGAAGAAAGCTTATTTATTTTCCCAACCTCCCCCAGGTGAGT 420
DB 361 CTGAGAGTCAGAGCTGAAGAAAGCTTATTTATTTTCCCAACCTCCCCCAGGTGAGT 420

QY 421 GTGACATATTTATTTAATACATCCACAAGAGATATTTTAAATATTTAAAGCATAA 480
DB 421 GTGACATATTTATTTAATACATCCACAAGAGATATTTTAAATATTTAAAGCATAA 480

QY 481 TATTTCTTAAAAAGTATTTAATATTTAAGTTGTGATGTTTAACTCTATCTGTCAT 540
DB 481 TATTTCTTAAAAAGTATTTAATATTTAAGTTGTGATGTTTAACTCTATCTGTCAT 540

QY 541 ACATCCTAGTGAATGTAATAATGCAAAATCCTGGTGAAGTGTCTTTGTTTGTCTTCT 600
DB 541 ACATCCTAGTGAATGTAATAATGCAAAATCCTGGTGAAGTGTCTTTGTTTGTCTTCT 600

QY 601 GTGAGCTCAACTAAGTTCACGGCCAAANGTCATGTTCTCCCTCTACCCNGTNGTAGTG 660
DB 601 GTGAGCTCAACTAAGTTCACGGCCAAANGTCATGTTCTCCCTCTACCCNGTNGTAGTG 660

QY 661 TTGTGGGGTCTCCTCCNTGGATCATCAAGGTGAACACTTAGGTATTTCTTTGGCAATCAGT 720
DB 661 TTGTGGGGTCTCCTCCNTGGATCATCAAGGTGAACACTTAGGTATTTCTTTGGCAATCAGT 720

QY 721 GCTCCTGTAACTCAAAATGTGTGCTTTGTACTGCTGTTGTTGAATGGANGTACTGTANA 780
DB 721 GCTCCTGTAACTCAAAATGTGTGCTTTGTACTGCTGTTGTTGAATGGANGTACTGTANA 780

QY 781 TAACTATGGAATTTTGAAGAAAAATTTCAAGAAAAAGAAAAATATATATTAATTTAAACTA 840
DB 781 TAACTATGGAATTTTGAAGAAAAATTTCAAGAAAAAGAAAAATATATATTAATTTAAACTA 840

QY 841 AAAAAAAAAAAAAAAAAA 856
DB 841 AAAAAAAAAAAAAAAAAA 856

RESULT 2
AAA74886
ID AAA74886 standard; DNA; 2738 BP.
XX
AC AAA74886;
XX
DT 17-JAN-2001 (first entry)
XX
DE Human chemokine MCP-2 coding sequence SEQ ID NO: 80.
XX
KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis; HIV;
KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; AIDS;
KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
KW basophil-mediated disease; myocardial infarction; acute ischaemia;
KW rheumatoid arthritis; contraception; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 123..356
FT /tag= a
FT /product= "human chemokine"
FT /transl_except= (pos:261..263,aa:Gln)
XX
PN WO200042071-A2.
XX
PD 20-JUL-2000.
XX
PF 12-JAN-2000; 2000WO-US00821.
XX
PR 12-JAN-1999; 99US-0229071.
PR 17-MAR-1999; 99US-0271192.
PR 01-DEC-1999; 99US-0452406.
XX
PA (NEOR-) NEORX CORP.
XX
PI Grainger DJ, Tatalick LM;
XX WPI; 2000-499101/44.
DR P-PSDB; AAB15786.
DR
XX
PT New peptide 3, amide and heterocyclic compounds and saccharide
PT conjugates used for inhibiting chemokine induced activity and for
PT treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
PT growth -
XX
PS Disclosure; Page 378-379; 387pp; English.
XX
CC The present invention concerns the identification of a number of
CC chemokines which can be used to produce derivatives, agonists and
CC antagonists which are then useful in disease treatment. The chemokines
CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
CC These chemokine derivatives can be used to treat diseases such as
CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated

21-MAR-2002.
17-SEP-2001; 2001WO-US29332.
15-SEP-2000; 2000US-232755P.
(GENA-) GENAISSANCE PHARM INC.
Anastasio AE, Chew A, Han J, Lee HH;
WPI: 2002-371973/40.
P-PSDB; ABG35167.
New genetic variants of Small Inducible Cytokine Subfamily A (Cys-Cys),
Member 8 (Monocyte Chemotactic protein) isogenes, useful for improving
efficiency and reliability in drug development for treating diseases
Claim 21; Fig 1; 84pp; English.
The present invention relates to novel single nucleotide polymorphisms
(SNPs) in the human small inducible cytokine subfamily A (Cys-Cys),
member 8 (monocyte chemotactic protein) (SCYA8) gene located on
chromosome 17, and methods for haplotyping and/or genotyping the SCYA8
gene. The methods of the invention make use of allele-specific
oligonucleotides (ASOs) as probes and primers and/or primer-extension
oligonucleotides for detecting the SCYA8 gene polymorphisms. The
polynucleotides and screened compounds are useful for the treatment of
diseases associated with SCYA8 activity, such as inflammatory diseases
and human immunodeficiency virus (HIV) infection. The present sequence
represents a reference sequence for the human SCYA8 gene which shows
the variations in the gene.

Sequence 9475 BP; 2863 A; 1898 C; 1777 G; 2925 T; 12 other;

Query Match	68.88;	Score 588.8;	DB 24;	Length 9475;
Best Local Similarity	97.88;	Pred. No. 8.4e-109;		
Matches 590; Conservative	2;	Mismatches 11;	Indels 0;	Gaps 0;

QY	238	ATCTCAAGACCAAAACGGGGCAAGGAGCTCTGTCTGACCCCCCAAGGAGAGATGGGTACAG	297
		: :	
Db	5369	AGCTTCAAGACCCMAACGGGGCAAGGAGKTCGTCTGACCCCCCAAGGAGAGATGGGTACAGG	5428
QY	298	GATTCCATGAAGCATCTGGAACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACAT	357
Db	5429	GATTCCATGAAGCATCTGGAACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACAT	5488
QY	358	GGACTGAGAGTCAGAGCTTGAAGAAAGCTTATTTATTTTCCCCAACCTCCCCCAGGTGC	417
Db	5489	GGACTGAGAGTCAGAGCTTGAAGAAAGCTTATTTATTTTCCCCAACCTCCCCCAGGTGC	5548
QY	418	AGTGTGACATTTATTTATTTATTAACATCCACAAAGAGATTTTTTAAATAATTAAAGCA	477
Db	5549	AGTGTGACATTTATTTATTTATTAACATCCACAAAGAGATTTTTTAAATAATTAAAGCA	5608
QY	478	TAAATATTTCTTAAAAAGTATTTAATTATATTAAAGTTGTGATGTTTAACTCTATCTGT	537
Db	5609	TAAATATTTCTTAAAAAGTATTTAATTATATTAAAGTTGTGATGTTTAACTCTATCTGT	5668
QY	538	CATACATCTCTAGTGAATGTAAAAATGCAAAATCCTGGTGATGTTTTTTTGTTTTGT	597
Db	5669	CATACATCTCTAGTGAATGTAAAAATGCAAAATCCTGGTGATGTTTTTTTGTTTTGT	5728
QY	598	CCTGTGAGCTCAACTAAGTTCACGGCCAAANGTCATTTGTTCTCCCTCCTACCGNTNGTA	657
Db	5729	CCTGTGAGCTCAACTAAGTTCACGGCCAAANGTCATTTGTTCTCCCTCCTACCTGTCTGTA	5788
QY	658	GTTGTGTGGGGTCTCCCNCTGGATCATCAAGGTGAACAACCTTAGGTATTTCTTTGGCAATC	717
Db	5789	GTTGTGTGGGGTCTCCCNCTGGATCATCAAGGTGAACAACCTTTGGTATTTCTTTGGCAATC	5848
QY	718	AGTGTCTCTGTAAGTCAAAATGTGTGCTTGTGTAAGTGTGTTGTTGAAATFGANGTTACTGT	777
Db	5849	AGTGTCTCTGTAAGTCAAAATGTGTGCTTGTGTAAGTGTGTTGTTGAAATFGANGTTACTGT	5908

QY	778	ANATACTATGGAATTTTGAAAAAAATTTCCAAAAAGAAAANA	TATATATTAATTAAAA	837
Db	5909	ATATAACTATGGAATTTTGAAAAAAATTTCAAAAAAGAAAAA	AATATATATATTAATTAAAA	5968
QY	838	CTA	840	
Db	5969	CTA	5971	

RESULT 4
AAT91023
ID AAT91023 standard; cDNA; 411 BP.

DT	16-FEB-1998 (first entry)
XX	
DE	Human beta-chemokine H1305 (MCP-2) cDNA

AA H1305; MCP-2; chemokine; human; chemottractant; chemotaxis;
 KW virus infection; HIV; therapy; wound healing; ds.
 KM

OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	47..376
FT		/*tag= a .

PN W09725427-A1.

PD 17-JUL-1997.

10-JAN-1997; 97WO-US00379.

PR 12-JAN-1996; 96US-0586395.

PA (GEMY) GENETICS INST INC.

PI Lavallie ER, McCoy JM, Racie LA;

DR WPI; 1997-372866/34.
DR P-PSDB; AAW26655.

PT treatment of viral infection, e.g. HIV, and in wound healing

PS Claim 1; Page 12-13; 21pp; English..

This novel isolated polynucleotide, the coding sequence of which is claimed, codes for human beta-chemokine H1305 (see AAW26655). A partial clone for H1305 was isolated from a human peripheral blood mononuclear cell (PBMC) cDNA library using methods that are selective for secreted proteins. The partial clone was then used to identify the full-length clone (deposited as ATCC 69968) from a PBMC library. Also claimed are: (1) a host cell, preferably mammalian, transformed with a H1306 polynucleotide operably linked to an expression control sequence; (2) a recombinantly produced H1305 protein; and (3) a composition comprising an antibody which specifically reacts with the H1305 protein. The H1305 protein (also known as MCP-2) may be used in a composition for the treatment of a mammalian subject (claimed). It is thought to have chemokine activities and may therefore have an effect on chemotaxis or migration of blood cells. It may be useful for inhibiting viral replication, including replication of HIV, and may also be used for treatment of wounds and to raise monoclonal and polyclonal antibodies which specifically react with H1305.

Sequence 411 BP; 116 A; 112 C; 93 G; 90 T; 0 other;

Query Match	44.28;	Score 378.4;	DB 18;	Length 411;
Best Local Similarity	99.78;	Pred. No. 7.3e-67;		
Matches 379;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

QY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAGATGAAGGTTTCTGCA 60
|||||
Db 32 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAGATGAAGGTTTCTGCA 91
QY 61 GCGCTTCTGTGCGCTGCTGCTCATGGCAGCCACTTTCAGCCCTCAGGAGACTTGCTCAGCCA 120
|||||
Db 92 GCGCTTCTGTGCGCTGCTGCTCATGGCAGCCACTTTCAGCCCTCAGGAGACTTGCTCAGCCA 151
QY 121 GATTCAAGTTTCCATTCCTCAATCACCCTGCTGCTTTAAGCTGATCAATAGCAAAATTCCTATC 180
|||||
Db 152 GATTCAAGTTTCCATTCCTCAATCACCCTGCTGCTTTAAGCTGATCAATAGCAAAATTCCTATC 211
QY 181 CAGAGGCTGGAGAGCTACACAGAATCACCAACATCCCAATGTCCCAAGGAAGCTGTGATC 240
|||||
Db 212 CAGAGGCTGGAGAGCTACACAGAATCACCAACATCCCAATGTCCCAAGGAAGCTGTGATC 271
QY 241 TTCAAGACCAAAACGGGCAAGAGGCTGTGCTGACCCCAAGGAGAGATGGCTCAGGGAT 300
|||||
Db 272 TTCAAGACCAAAACGGGCAAGAGGCTGTGCTGACCCCAAGGAGAGATGGCTCAGGGAT 331
QY 301 TTCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGA 360
|||||
Db 332 TTCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGA 391
QY 361 CTGAGAGTCAGAGCTTGAAG 380
|||||
Db 392 CTGAGAGTCAGAGCTTGAAG 411

RESULT 5
AAF21017
ID AAF21017 standard; DNA; 1085 BP.
XX
AC AAF21017;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2584.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
XX
PS Disclosure; Page 829; 1592pp; English.

XX
CC The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with CC lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, CC immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, CC binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system CC receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and CC receptors, binding proteins and malignancy associated proteins. The CC antisense oligonucleotides may be used in this way to treat disorders CC including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) CC and/or surfactant hypoproduction which are associated with a disease or CC condition selected from pulmonary vasoconstriction, inflammation, CC allergies, asthma, impeded respiration, respiratory distress syndrome CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD), CC pulmonary transplantation rejection, pulmonary infections, bronchitis, CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide CC fragments and antisense oligonucleotides used in the exemplification of CC the present invention.

XX
SQ Sequence 1085 BP; 314 A; 214 C; 229 G; 328 T; 0 other;

Query Match 30.1%; Score 257.6; DB 21; Length 1085;
Best Local Similarity 67.9%; Pred. No. 1.5e-42;
Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;

QY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAGATGAAGGTTTCTGCA 60
|||||
Db 284 AAACCTTCACCTCTCATGCTGAAGGCCATGCCCTCACCCCTCCACATGAAGGCTTGTGCA 343
QY 61 GCGCTTCTGTGCGCTGCTGCTCATGGCAGCCACTTTCAGCCCTCAGGAGACTTGCTCAGCCA 120
|||||
Db 344 GCACCTTCTGTGCTGCTGCTCATCAGCAGAGCTGCTTTCAGCCCCCAGGGGCTTGCTCAGCCA 403
QY 121 GATTCAAGTTTCCATTCCTCAATCACCCTGCTGCTTTAAGCTGATCAATAGCAAAATTCCTATC 180
|||||
Db 404 GTTGGATTAACTTCACTCACTACCTGCTGCTACAGATTATCAATAGAAATCCCTAAG 463
QY 181 CAGAGGCTGGAGAGCTACACAAGAATCACCAACATCCCAATGTCCCAAGGAAGCTGTGATC 240
|||||
Db 464 CAGAGGCTGGAGAGCTACACAAGAAGCACCAAGCAGTACGACCTGCCCCGGAAGCTGTATTC 523
QY 241 TTCAAGACCAAAACGGGCAAGAGGCTGTGCTGACCCCAAGGAGAGATGGGTCAGGGAT 300
|||||
Db 524 TTCAAGACCAAAACGGGCAAGAGATCTGTGCTGACCCCAAGGAGATGGGTCAGGGAT 583
QY 301 TTCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGA 360
|||||
Db 584 TTTATGAAGCACCCTGGACAAGAAAACCCAAACTCCAAAGCTTTGAACATTCATGACTGA 643
QY 361 CTGAG---AGTCAGAGCTTGAAGAAAAGCTTATTTATTTTCCCAACCTCCCCCAGGTG 416
|||||
Db 644 CTGAACAACAGCCATGACTTGAGAAAACAATTAATTTGTATTAACCTGTCTTCAGAGT 703
QY 417 CAGTGTGACATTTATTTATTAACATCCACAAGA-GATTATTTTAAATTAATTTAAG 475
|||||
Db 704 GGTTCGAGATTAATTTATCTAATTTCTAAGGAATATGAGCTTTATGTAATAATGTGAAT 763
QY 476 CATATATTTCTTAAAGATTTAATTAATTAATTTAAGTGTGATGTTTAACTCTATCT 535
|||||
Db 764 CATGTTTCTTAGTAGATTTTAA-----AAGTTATTAATTAATTTAATTTAATCT 814

OY	536	GT	CATACATCTT	AGTGAATGTA	AAATGC	AAAAATCC	TGTCATGTC	TTT	TTT	TTT	TTT	GTT	595
Db	815	TCCATG	GATTTT	GTGGCTTT	TGAACATAA	AGCCCTT	GGATGTA	TATATG	TCATCTC	AGTGCT			874
OY	596	TT	597										
Db	875	GT	876										
RESULT	6												
AAF21018													
ID	AAF21018	standard;	DNA;	1085	BP.								
XX													
AC	AAF21018;												
DT	14-MAR-2001	(first entry)											
XX													
DE	Human	low	adenosine	antisense	oligonucleotide	related	sequence	#2585.					
KW	Low	adenosine	antisense	oligonucleotide;	phosphorothioate;	allergy;							
KW	human;	airway	disorder;	bronchoconstriction;	lung	inflammation;							
KW	surfactant	depletion;	respiratory;	bronchodilator;	antiinflammatory;								
KW	immunosuppressive;	asthmatic;	analgesic;	hypotensive;	cytostatic;								
KW	respiratory	obstruction;	pulmonary	obstruction;	impeded	respiration;							
KW	surfactant	hypoproduction;	pulmonary	vasoconstriction;	asthma;	RDS;							
KW	respiratory	distress	syndrome;	pain;	cystic	fibrosis;	allergic	rhinitis;					
KW	pulmonary	hypertension;	emphysema;	pulmonary	transplantation	rejection;							
KW	chronic	obstructive	pulmonary	disease;	pulmonary	infection;	bronchitis;						
KW	cancer;	ss.											
XX													
OS	Homo	sapiens.											
XX													
PN	MO200062736-A2.												
XX													
PD	26-OCT-2000.												
XX													
PF	24-MAR-2000;	2000WO-US08020.											
XX													
PR	06-APR-1999;	99US-0127958.											
XX													
PA	(UYEC-) UNIV	EAST CAROLINA.											
PA	(NYCE/) NYCE	J W.											
XX													
PI	Nyce	JW;											
XX													
DR	WPI;	2000-679539/66.											
XX													
PT	Low	adenosine (A)	content	antisense	oligonucleotides	which	do	not					
PT	trigger	adenosine	receptors	during	metabolism,	useful	e.g.	for	treating				
PT	cancers	and	respiratory	obstructions	-								
PS													
PS	Disclosure;	Page	829-830;	1592pp;	English.								
XX													
CC	The	present	invention	describes	low	adenosine	(A)	content	antisense				
CC	oligonucleotides	and	compositions	(I)	comprising	them.	In	the	antisense				
CC	oligonucleotides	the	A	is	replaced	by	a	'universal'	or	alternative	base		
CC	(I)	can	have	respiratory,	bronchodilator,	antiinflammatory,	analgesic,						
CC	immunosuppressive,	antiasthmatic,	hypotensive	and	cytostatic	activities							

CC	and/or surfactant hypoproduction which are associated with a disease or
CC	condition selected from pulmonary vasoconstriction, inflammation,
CC	allergies, asthma, impeded respiration, respiratory distress syndrome
CC	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC	and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC	fragments and antisense oligonucleotides used in the exemplification of
CC	the present invention.
XX	
SO	Sequence 1085 BP; 314 A; 214 C; 229 G; 328 T; 0 other;
	Query Match 30.1%; Score 257.6; DB 21; Length 1085;
	Best Local Similarity 67.9%; Pred. No. 1.5e-42;
	Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;
OY	1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCTTGCCCTCCAGATGAAGTTCTGCA 60
DB	284 AACCTCCAATTCTCATGTGGAAGCCCCATGCCCTCACACCTGAAGAAGCCTGCA 343
OY	61 GCCCTTCTGTGCCTGCTGCTCATGGCAGCCACTTTCAGCCCTTCAGGGACTTGCTCAGCCA 120
DB	344 GCACCTCTGTGTCTGTCTCTCACAGCAGCTGCTTTCAGCCCCCAGGGGGCTTGCTCAGCCA 403
OY	121 GATTTCAGTTTCCATTCCAAATCACCTGCTGCTTTAAGTGATCAATAGGAATAATTCCTATC 180
DB	404 GTTGGATTATTACTTCAACTAACCTGCTGCTACAGATTATTAAGAAATCCCTAAG 463
OY	181 CAGAGGCTGAGAGCTACACAAGAATCACCAACATCCAAATGTCCTCAAGGAAGCTGTGATC 240
DB	464 CAGAGGCTGAGAGCTACAGAGGAGCAACCAAGTAGCCACTGTCCCAGGAAGCTGTATC 523
OY	241 TTCAAGACCAAACGGGGCAGAGAGTCTGTGCTGACCCCAAGAGAGATGGGTGAGGAT 300
DB	524 TTCAAGACCAAACCTGGACAGAGATCTGTGCTGACCCCAAGAGAGATGGGTGAGGAC 583
OY	301 TTCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 360
DB	584 TTATGAAGCACCCTGGACAAAGAAACCCAAACTCCAAAGCTTGAACATTCATGACTGAA 643
OY	361 CTGAG----AGTCAGAGCTTGAAGAAAAGCTTATTTATTTTCCCAACCTCCCCAGGTG 416
DB	644 CTGAACAACAGCCATGACTTGAGAAACAATAATATTGTATACCTGTCCTTCTCAGAGT 703
OY	417 CAGTGTGACATTATTTATTAATCAATCCACAAAGA-GATTATTTTTAATAATTTAAG 475
DB	704 GGTCTGAGATTATTTAATCTAATTTCTAAGGAATATGAGCTTATGTAATAATGTGAAT 763
OY	476 CATATATTTCTTAAAAAGATTTAATTTATATTTAAGTTGTTGATGTTTAACTCTATCT 535
DB	764 CATGCTTTTCTTAGTAGATTTAA-----AAGTTATTAATTTAATTTAATCT 814
OY	536 GTCATACATCTAGTGAATGTAAATGCAAAATCCTGGTGAATGTTTTTTGTTTGT 595
DB	815 TCATGATGATTTTGGTGGGTTTGAACATAAAGCCTTGATGTATATGTCACTCAGTGCT 874
OY	596 TT 597
DB	875 GT 876
RESULT 7	
ID	AAA74887 standard; DNA; 1085 BP.
XX	
AC	AAA74887;
XX	
DT	17-JAN-2001 (first entry)
DE	Human chemokine MCP-3 coding sequence SEQ ID NO: 81.
KW	Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
XX	monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;

CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONS reduces side effects. The A-containing ONS break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONS from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
XX
SQ Sequence 1085 BP; 314 A; 214 C; 229 G; 328 T; 0 other;

Query Match 30.1%; Score 257.6; DB 21; Length 1085;
Best Local Similarity 67.9%; Pred. No. 1.5e-42;
Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;

OY 1 AAACCTCACCTCTCATGCTGAGCTCACACCCCTGCCCTCCAGATGAAGCTTCTGCA 60
DB 284 AAACCTCCAATCTCATGTGGAAGCCCATGCCCTCACCTCCACATGAAGCCTCTGCA 343
OY 61 GCGCTCTGTGCTGCTGCTCATGGCAGCCACTTTCAGCCCTCAGGACTTGCTCAGCCA 120
DB 344 GCACCTTCTGTGCTGCTGCTCATGAGCAGCAGCTGCTTTCAGCCCTCAGGCTGCTCAGCCA 403
OY 121 GATTCAGTTTCCATTCATCACCCTGCTGCTTAAAGTGATCAATAGAGAAAATTCCTATC 180
DB 404 GTTGGGATTAATACTTCAACTACCTGCTGCTACAGATTATCAATAAGAAAATCCCTAAG 463
OY 181 CAGAGGCTGGAGAGCTACACAGAATCACCAATCCAAATGTCCCAAGAGAGCTGTGATC 240
DB 464 CAGAGGCTGGAGAGCTACACAGAAGCACCACCACTGACCTGCCCGGAAGCTGTAATC 523
OY 241 TTCAAGACCAAAAGGGGCAAGAGGTCTGTGCTGAGCCCAAGAGAGATGGGTCAAGGAT 300
DB 524 TTCAAGACCAAACTGGACAGAAGAGATCTGTGCTGAGCCCAACACAGAGAAGTGGGTCCAGGAC 583
OY 301 TCCATGAAGCATCTGGACCAAAATATTTCAAAATCTGAAGCCATGAGCCTTCATCATGGA 360
DB 584 TTTATGAAGCACCTGGACAGAAGAAAACCAACTCCAAAGCTTGAACATTCATGACTGAA 643
OY 361 CTGAG---AGTCAGAGCTTGAAGAAAAGCTTATTTTCCCAACCTCCCCAGGTG 416
DB 644 CTGAAAACAAGCCATGACTTGAGAAAACAATTAATTGTATACCCTGTCTTCTTCAGAGT 703
OY 417 CAGTGTGACATTAATTTTATTAACATCCACAAGA-GATTATTTTAAATTAATTAAAG 475
DB 704 GGTCTGAGATTATTTTAATCTAATCTAAGGAAATATGAGCTTATGTAATATGTAAT 763
OY 476 CATAATATTTCTTAAAGATATTTAATATTAAGTTGTGATGTTTAACTCTATCT 535
DB 764 CATGGTTTCTTCTAGATTTTAA-----AAGTTATTAATTTTAACTCTATCT 814
OY 536 GTCATACATCTAGTGAATGTAATGCAAAATCCTGGTGATGTGTTTGTGTTTGT 595
DB 815 TCCATGGAATTTGGTGGTTTGAACATAAAGCCTTGATGTATATGTCATCTCAGTGCT 874
OY 596 TT 597
DB 875 GT 876

RESULT 9

AAA34896
ID AAA34896 standard; DNA; 1085 BP.
XX
XX AAA34896;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2585.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.
XX
XX WO200009525-A2.
XX
XX 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17712.
XX
XX 03-AUG-1998; 98US-0095212.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX NYce JW;
XX
XX WPI; 2000-205971/18.

PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
XX

PS Disclosure; Page 759; 1343pp; English.

XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONS reduces side effects. The A-containing ONS break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONS from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

XX
SQ Sequence 1085 BP; 314 A; 214 C; 229 G; 328 T; 0 other;
Query Match 30.1%; Score 257.6; DB 21; Length 1085;
Best Local Similarity 67.9%; Pred. No. 1.5e-42;
Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;

QY 1 AACCTTCACCTCTCATGCTGAAGCTCACACCCTTGCCCTCCAAGATGAAGTTTCTGCA 60
||||| 11 111111 1111 11 111 111111 1111 1 11111
Db 284 AAACCTCCAATTCATGTGGAGAGCCCATGCCCCCTCACCCCTCCACATGAAGCCCTCTGCA 343
QY 61 GCGCTTCTGTGCGCTGCTCATGCGACGCCACTTTCAGCCCTCAGGGACTTGCTCAGCCA 120
|| 11111111 11111111 1111 11111111 1111 1111111111
Db 344 GCACCTTCTGTGCTGCTGCCTCAGACAGAGCTGCTTTCAGCCCCCAGGGGCTTGCTCAGCCA 403
QY 121 GATTGAGTTTCCATTCACATGACCTGCTGCTTTAACGTGATCAATGAGAAATTCCTATC 180
|| 11 11 111 11111111 11 111111 11111 1111 1111
Db 404 GTTGGATTAACTTCAACTGACCTGCTGCTACAGATTATCAATTAAGAAATCCCTAAG 463
QY 181 CAGAGGCTGAGAGCTACACAGAATCACCAACATCCAATGTCCCAAGAGAGCTGTGATC 240
||||| 11111111 1111 1111 1111 1111 111111 11111111 111
Db 464 CAGAGGCTGAGAGCTACAGAGAGCACCAGTAGAGCCACTGTCCCGGGAAGCTGTAATC 523
QY 241 TTCAAGACCAACAGGGGCAAGAGAGTCTGTGCTGACCCCAAGAGAGATGGGTGAGGAT 300
||||| 111111 11 111111 111111111111 11 11111 111
Db 524 TTCAAGACCAAACTGGACAGAGATCTGTGCTGACCCACACAGAGAGTGGGTCCAGGAC 583
QY 301 TCCATGAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGCA 360
1 111111 111111 11 1111 11 1111 111 11111 111
Db 584 TTTATGAAGCACCCTGGACAGAAACCCTCAAGCTTTGAACATTCATGACTGAA 643
QY 361 CTGAG---AGTCAGAGCTGGAAGAAAGCTTATTATTTCGCCAACCTCCCGCAGGTG 416
||||| 11 11 11111 11 1111 11 1111 111 111
Db 644 CTGAAACAACAGCCATGACTGTGAGAAACAATAATTTGTATACCTGTCTTCAGAGT 703
QY 417 CAGTGTGACATTTATTTATTAACATCCACAAAGA-GATTATTTTAAATTAATTAAG 475
1 111 11111111 1111 11 11 11 11111 111
Db 704 GGTTCGAGATTTATTTAATCTAATCTAAGAAATATGAGCTTTATGTAATATGTAAT 763
QY 476 CATATATTTCTTAAAGATTTAATTTATTTAAGTGTGATGTTTAACTCTATCT 535
111 1 111111 1 111 11111 11 111111 1 1111
Db 764 CATGTTTCTTCTAGTAGATTTTAA-----AAGTTATTAATTTTAACTTATCT 814
QY 536 GTCATACATCTAGTGAATGTAATAATGCAAAATCCTGATGATGTTTTTTGTTTGT 595
111 11 1111 1 11 11 111 111 111 11 11 111
Db 815 TCCATGATTTTGGTGGGTTTGAACATTAAGCCTTGATGTATATGTCATCTCAGTGCT 874
QY 596 TT 597
1
Db 875 GT 876
Db 875 GT 876

RESULT 10
ABK84649
ID ABK84649 standard; cDNA; 1085 BP.
XX
AC ABK84649;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #1220.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30821.
XX
PR 03-OCT-2000; 2000US-237189P.

XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity
XX
PS Claim 1; SEQ ID NO 1220; 114p; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression (M2) GA by contacting GC with an agent
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1085 BP; 314 A; 214 C; 229 G; 328 T; 0 other;

Query Match 30.1%; Score 257.6; DB 24; Length 1085;
Best Local Similarity 67.9%; Pred. No. 1.5e-42;
Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;

QY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCTTGCCCTCCAAGATGAAGTTTCTGCA 60
||||| 11 111111 1111 11 111 111111 1111 1 11111
Db 284 AAACCTCCAATTCATGTGGAGAGCCCATGCCCCCTCACCCCTCCACATGAAGCCCTCTGCA 343
QY 61 GCGCTTCTGTGCGCTGCTCATGCGACGCCACTTTCAGCCCTCAGGGACTTGCTCAGCCA 120
|| 11111111 11111111 1111 11111111 1111 1111111111
Db 344 GCACCTTCTGTGCTGCTGCCTCAGACAGAGCTGCTTTCAGCCCCCAGGGGCTTGCTCAGCCA 403
QY 121 GATTGAGTTTCCATTCACATGACCTGCTGCTTTAACGTGATCAATGAGAAATTCCTATC 180
|| 11 11 111 11111111 1 111111 11111 1111 1111
Db 404 GTTGGATTAACTTCAACTGACCTGCTGCTACAGATTATCAATAAGAAATCCCTAAG 463
QY 181 CAGAGGCTGAGAGCTACACAGAATCACCAACATCCAATGTCCCAAGAGAGCTGTGATC 240
||||| 11111111 111111 11 1111 1 11 11111 11111111 111
Db 464 CAGAGGCTGAGAGCTACAGAGAGCACCAGTAGAGCCACTGTCCCGGGAAGCTGTAATC 523

OY	241	TTCAAGACCAAACGGGGAAGAGCGTCTGTGCTGCACCACAAGAGAGATGGGTCAAGGAT	300
Db	524	TTCAAGACCAAACACTGGACAAGAGATCTGTGCTGCACCACACAGAAGTGGGTCCAGGAC	583
OY	301	TCCATGAAGCATCTGGACCCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA	360
		-	
Db	584	TTTATGAAGCACCTTGACAAGAAAAACCCTCAAAAGCTTTGAACATTCATGACTGAA	643
OY	361	CTGAG---AGTCAGAGCTTGAAGAAAAGCTTATTATTTTCCCCAACCTCCCAGGTG	416
Db	644	CTGAAAACAAGCCATGACTGAGAAACAATAATTGTATACCCGTGCCCTTCCAGAGT	703
OY	417	CAGTGTGACATTATTTTATTATTAACATCCACAAGA-GATTATTTTTAATAATTTAAG	475
		-	
Db	704	GGTCTGAGATTATTTAATCTAATCTAAGGAATATGAGCTTATGTAAATATGTGAAT	763
OY	476	CATAATATTTCTTAAAAAGTATTAAATTATTTAAGTGTGTGATGTTTAACTCTATCT	535
Db	764	CATGGTTTTTCTTAGTAGATTTTAA-----AAGTTATTAAATATTTTAAATTAACTCT	814
OY	536	GTCATACATCCTAGTGAATGTAAAAATGCAAAATCCTGCTGATGTGTTTTTGTGTT	595
Db	815	TCCATGGATTTTGGTGGGTTTGAACATAAGCCCTTGATGTATATGTCAATTCAGTGTCT	874
OY	596	TTT 597	
		-	
Db	875	GT 876	

```

RESULT 11
AAS44714
ID AAS44714 standard; DNA; 1706 BP.

```

AC AAS44714;

DT 18-DEC-2001 (first entry)

Full-length polynucleotide sequence #139.

KW Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW nervous system disorder; inflammatory disorder; cell differentiation; ds;
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW cytosolic; antirheumatic; antiarthritic; vulnery; antiinflammatory;
KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
KW neuroprotective; osteopathic; antidiabetic; antiallergic;
KW immunostimulant; analgesic; gene therapy.

OS Unidentified.

PN WO200164834-A2.

PD 07-SEP-2001.

26-FEB-2001; 2001WO-US049226.

PR 28-FEB-2000; 2000US-0515126.

PR 17-JUN-2000; 2000US-0597707.

19-SEP-2000; 2000US-0664641.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C,

PI	Dimanac R;	Wahmanan 2/	Wahng 3/	Wahng 4/	Ornan 10/	Wahng 5/
1	100	100	100	100	100	100
2	100	100	100	100	100	100
3	100	100	100	100	100	100
4	100	100	100	100	100	100
5	100	100	100	100	100	100
6	100	100	100	100	100	100
7	100	100	100	100	100	100
8	100	100	100	100	100	100
9	100	100	100	100	100	100
10	100	100	100	100	100	100
11	100	100	100	100	100	100
12	100	100	100	100	100	100
13	100	100	100	100	100	100
14	100	100	100	100	100	100
15	100	100	100	100	100	100
16	100	100	100	100	100	100
17	100	100	100	100	100	100
18	100	100	100	100	100	100
19	100	100	100	100	100	100
20	100	100	100	100	100	100
21	100	100	100	100	100	100
22	100	100	100	100	100	100
23	100	100	100	100	100	100
24	100	100	100	100	100	100
25	100	100	100	100	100	100
26	100	100	100	100	100	100
27	100	100	100	100	100	100
28	100	100	100	100	100	100
29	100	100	100	100	100	100
30	100	100	100	100	100	100
31	100	100	100	100	100	100
32	100	100	100	100	100	100
33	100	100	100	100	100	100
34	100	100	100	100	100	100
35	100	100	100	100	100	100
36	100	100	100	100	100	100
37	100	100	100	100	100	100
38	100	100	100	100	100	100
39	100	100	100	100	100	100
40	100	100	100	100	100	100
41	100	100	100	100	100	100
42	100	100	100	100	100	100
43	100	100	100	100	100	100
44	100	100	100	100	100	100
45	100	100	100	100	100	100
46	100	100	100	100	100	100
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55	100	100	100	100	100	100
56	100	100	100	100	100	100
57	100	100	100	100	100	100
58	100	100	100	100	100	100

DR WPI; 2001-589862/66.

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PT Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis, treatment of
PT cancer, neurological, inflammatory disorders and for use in arrays for
PT detection -

PS Claim 1; SEQ ID NO 139; 153pp; English.

CC Sequences AAS44576-AAS44919 represent full-length polynucleotides and
CC contig polynucleotides encoding polypeptides of the invention. The DNA
CC and protein sequences are useful for the treatment, diagnosis and
CC prevention of various types of disorder in a mammalian subject such as a
CC human, dog, monkey, mouse, hamster or rat. The disorders include cancers
CC such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
CC bowel disease. The sequences exhibit activity relating to angiogenesis,
CC cell proliferation, cell differentiation, stem cell growth factor,
CC activin or inhibin. Therefore, they can be used to manipulate stem cells
CC in culture to give rise to neuroepithelial cells that can be used to
CC augment or replace cells damaged by illness, accidental damage or genetic
CC disorders. The sequences may also be used for regeneration of bone,
CC cartilage, tendons and ligaments and in tissue repair and burn healing.
CC Note: Some sequences for this patent did not form part of the printed
CC specification, but were obtained in electronic format directly from WIPO
CC at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 1706 BP; 447 A; 333 C; 392 G; 534 T; 0 other;

Query Match 30.18; Score 257.6; DB 22; Length 1706;

Best Local Similarity 07:28; 1400; NO: 1:00 12;
Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;

QY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAAGATGAAGTTTCTGCA 60

Db 905 AAACCTCCAATTCTCATGTGGAGCCCATGCCCTCACCTCCACACATGAAGCCTCTGCA 964

61 GCGCTTCTGTGCGCTGCTCATGGCAGCCACTTTCAGCCCTCAGGACTTGCTCAGCCA 120

Db 965 GCACCTCTGTGTCCTGCTCACAAGCAGCTGCTTTCAGCCCCCAGGGGCTTGCTCAGCCA 102

QY 121 GATTCAGTTTCCATTCCCAATCACCCTGCTGCTTTAACGTGATCAATAGGAAATTCTATC 1800

Db 1025 GTTGGGATTAACTACTTCACTACCTGCTGCTACAGATTATCAATAGAAATCCCTAAG 108

QY 181 CAGAGGCTGGAGAGCTACACAAGAATCACCAACATCCAATGTCCCAAGGAAGCTGTGATC 240

Db 1085 CAGAGGCTGAGAGCTACAGAAGGACCACCACTAGCCACTGTCCCGGGAAGCTGTAATC 114

241 TTCAGACCAACGGGGCAAGGAGTCTGTCTGACCCCAAGGAGATGGGTCAGGAT 300

Db 1145 TTCAAGACCAACTGGACCAAGGAGATCTGTGCTGACCCACACAGAAGTGGGTCCAGGAC 1200

301 TCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGA 360

Db 1205 TTTATGAAGCACCTGGACAAGAAACCCCAACTCCAAAGCTTGAACATTCATGACTGAA 126

361 CTGAG---AGTCAGAGCTTGAAGAAAGCTTATTATTTCGCCCAACCTCCCCCAGGTC 416

Db 1265 CTGAACAACGCCATGACTTGAGAAACAATAATTGTATACCCCTGTCCTTCTCAGAGT 132

417 CAGTGTGACATTATTTTATTATTAACATCCACAAGA-GATTATTTTAAATAATTAAAG 475

Db 1325 GGTCTGAGATTATTTAATCTAATCTAAGGAATATGAGCTTTATGTAATAATGTGAAT 1330

QY 476 CATAATATTTCTTAAAAAGTATTTAATTATTTTAAGTTGTCATGTTTAACTCTATCT 535

Db 1385 CATGTTTCTCTAGTAGATTAA-----AAGTTATTAATTTTAATTAAATCT 14385

536 GTCATACATCCTAGTGAATGTAATAAGCAAAATCCTGGTGATGTTT 595

Db 1436 TCCATGGATTGTTGGTGGTTTGAACATAAGCCTTGATGTATATGTCATCTCAGTGCT 1495
QY 596 TT 597
+
Db 1496 GT 1497

RESULT 12
AAAF21020
ID AAF21020 standard; DNA; 5865 BP.
XX
AC AAF21020;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2587.
XX
KM Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
XX (NYCE/) NYCE J W.
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX
PS Disclosure; page 831-832; 1592pp; English.

CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or

CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 5865 BP; 1675 A; 1286 C; 1183 G; 1721 T; 0 other;

Query Match 30.1%; Score 257.6; DB 21; Length 5865;
Best Local Similarity 67.9%; Pred. No. 2.1e-42;
Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;

QY 1 AAACCTTACCTCTCATGCTGAAGCTCACACCTTGCCCTCCAAGATGAAGGTTTCTGCA 60
+
Db 1094 AAACCTTCAATTCTCATGTGGAAGCCCATGCCCTCACCTCCAACATGAAGCCTCTGCA 1153

QY 61 GCGCTTCTGTCCTGCTGCTCATGCGAGCCACTTTCAGCCCTCAGGGAGTGTGCTCAGCCA 120
+
Db 1154 GCACCTTCTGTGTCTGCTGCTCACAGACGCTGTTTCAGCCCCAGGGGCTGCTCAGCCA 1213

QY 121 GATTCAAGTTTCCATTCATCACCTGCTGCTTTAAGTGATCAATAGAAATTCCTATC 180
+
Db 1214 GTTGGATTAATTAATCTCAACTACCTGCTGCTACAGATTATCAATAAGAAATCCCTAAG 1273

QY 181 CAGAGCGTGAAGCCTACACAGAATCACCAATCCAAATGTCGCCAAGAGAGCTGTGATC 240
+
Db 1274 CAGAGCGTGAAGCCTACAGAAAGACCAACCACTGATCCCGGGAAGCTGTATATC 1333

QY 241 TTCAAGACCAAAAGGGGCAAGAGGCTGTGCTGACCCCAAGAGAGATGGGTACAGGAT 300
+
Db 1334 TTCAAGACCAAAAGTGAACAAGAGATGTGTGACCCCAACAGAGTGGGTCCAGGAC 1393

QY 301 TCCATGAAGCATCTGGAACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGA 360
+
Db 1394 TTTATGAAGCACTGGAACAAGAAACCAACCTCAAAAGCTTTGAACATTCATGACTGAA 1453

QY 361 CTGAG---AGTCAGAGCTTGAAGAAAGCTTATTTTCCCAACCTCCCCAGGTG 416
+
Db 1454 CTGAACAACAGCCATGACTTGAGAACAATATTTGTATACCTGTCTTCACAGAT 1513

QY 417 CAGTGTGACATTTATTTATATACATCCACAAGA-GATTATTTTAAATTAATTAAAG 475
+
Db 1514 GGTTCAGATTAATTTTAACTAATCTAATCTAAGCAATATGAGCTTATGTAAATGCTGAAT 1573

QY 476 CATAATATTTCTTAAAGATATTTAATTAATTAAGTTGTGATGTTTAACTATCT 535
+
Db 1574 CATGTTTCTTCTAGATTTTAA-----AAGTTATTAATATTTTAAATCT 1624

QY 536 GTCATACATCCTAGTGAATGTAAATGCAAAATCCCTGCTGATGTGTTTGTGTT 595
+
Db 1625 TCCATGGATTGTTGGTGGTTTGAACATAAAGCCTTGATGTATATGTCATCTCAGTGCT 1684

QY 596 TT 597
+
Db 1685 GT 1686

RESULT 13
AAA34898
ID AAA34898 standard; DNA; 5865 BP.
XX
AC AAA34898;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2587.
XX
KM Human; adenosine receptor; low adenosine antisense oligonucleotide;
KM phosphorothioate; impaired respiration; inflammation; allergy;
KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

PT cancers and respiratory obstructions -
XX.
PS Disclosure; Page 829; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
XX Sequence 810 BP; 248 A; 169 C; 155 G; 238 T; 0 other;

Query Match 29.9%; Score 256; DB 21; Length 810;
Best Local Similarity 67.8%; Pred. No. 3e-42;
Matches 408; Conservative 0; Mismatches 180; Indels 14; Gaps 3;

QY 1 AAACCTTCACCTCTCATGCTGAAGCTCAACCCCTTGCCCTCAAGATGAAGTTCTGCA 60
DB 26 AAACCTCCAATTCATGTGGAAGCCCATGCCCTCACCTCCAACATGAAGCCTCTGCA 85
QY 61 GCGCTTCTGTGCTGCTCATGCGACGCCACTTTACGCCCTCAGGACTTGCTCAGCCA 120
DB 86 GCACTTCTGTGTGCTGCTCAGACAGAGCTGCTTCAAGCCCCAGGGGCTGCTCAGCCA 145
QY 121 GATTCAGTTTCCATTCACATCAGCTGCTGTTAACGTCATCAATAGAAAATTCCTATC 180
DB 146 GTTGGATTAACTACTCAACTGCTGCTACAGATTATTCATTAAGAAAATCCCTAAG 205
QY 181 CAGAGGCTGGAGAGCTACACAGAATCACCAACATCCAATGTCCCAAGAGGCTGTGATC 240
DB 206 CAGAGGCTGGAGAGCTACAGAGAAGACCACAGTAGCCACTGTCCCGGAAGCTGTAATC 265
QY 241 TTCAAGACCAAAACGGGCAAGAGTCTGTGCTGACCCCAAGAGAGATGGTCAGGAT 300
DB 266 TTCAAGACCAAACTGACAGAGAGATCTGTGCTGACCCACACAGAGATGGTCCAGGAC 325
QY 301 TCCATGAAGCATCTGACCAATATTTCAAAATCTGAAGCATGAGCCTCATACATGA 360
DB 326 TTTATGAAGCACCTGACAGAAAACCCAAACTCCAAGCTTTGAACATTCATGACTGAA 385
QY 361 CTGA---GAGTCAGAGCTTGAAGAAAAGCTTATTTATTTTCCCAACCTCCCCAGGTG 416
DB 386 CTAAAAACAAGCCATGACTTGAGAAACAATTAATTTGTATACCTGTCTTCTCAGAGT 445
QY 417 CAGTGTGACATATTTATTTATTAACATCCACAAGA-GATTATTTTAAATATTTAAAG 475
DB 446 GGTCTGAGATTATTTATCTAATTTCTAAGGAATATGAGCTTTATGTATATATGTGAAT 505
QY 476 CATATATTTCTTAAAAAGTATTTAATTAATTAATTTAAGTTGTGATGTTTAACTCTATCT 535

DB 506 CATGGTTTCTTCTAGTAGATTTAA-----AAGTTATTAATTTTAATTAATCT 556
QY 536 GTCATACATCCTAGTGAATGTAATAATGCAAAATCCTGTCGATGCTGTTTGTGTTTGT 595
DB 557 TCCATGGAATTTTGGTGGTTTGAACATAAAGCCTTGATGTATATGTCATCTCAGTGCT 616
QY 596 TT 597
DB 617 GT 618
RESULT 15
AAA34894
ID AAA34894 standard; DNA; 810 BP.
XX
AC AAA34894;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2583.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 758; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONS reduces side effects. The A-containing ONS break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last

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OM nucleic - nucleic search, using sw model

Run on: February 17, 2003, 23:54:35 ; Search time 56 Seconds
(without alignments)
4687.773 Million cell updates/sec

Title: US-10-033-067-2
Perfect score: 856
Sequence: 1 aaacctcaccctcatgct.....actaaaaaaaaaaaaaa 856

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256	29.9	814	3 US-07-927-391-15	Sequence 15, Appl
2	233.2	27.2	605	4 US-09-366-887A-26	Sequence 26, Appl
3	219.8	25.7	741	3 US-07-927-391-25	Sequence 25, Appl
4	201	23.5	752	6 5212073-1	Patent No. 5212073
5	183.6	21.4	540	4 US-08-744-419-1	Sequence 1, Appl
6	170.4	19.9	297	4 US-08-613-822-3	Sequence 3, Appl
7	170.4	19.9	297	4 US-08-852-212-1	Sequence 1, Appl
8	170.4	19.9	297	4 US-09-479-729B-3	Sequence 3, Appl
9	170.4	19.9	297	4 US-09-261-201A-3	Sequence 3, Appl
10	163.2	19.1	315	4 US-08-744-419-3	Sequence 3, Appl
11	156.8	18.3	994	4 US-09-366-887A-5	Sequence 5, Appl
12	153.6	17.9	818	4 US-09-366-887A-15	Sequence 15, Appl
13	139.2	16.3	247	3 US-07-927-391-17	Sequence 17, Appl
14	138	16.1	228	3 US-07-927-391-13	Sequence 13, Appl
15	137.4	16.1	228	1 US-08-250-958-3	Sequence 3, Appl
16	137.4	16.1	231	5 PCT-US95-00605-2	Sequence 2, Appl
17	96.6	11.3	207	4 US-09-463-458A-28	Sequence 28, Appl
18	95.2	11.1	207	4 US-09-463-458A-8	Sequence 8, Appl
19	95.2	11.1	207	4 US-09-463-458A-25	Sequence 25, Appl
20	91.8	10.7	353	4 US-09-366-887A-21	Sequence 21, Appl
21	84.2	9.8	151	4 US-09-366-887A-17	Sequence 17, Appl
22	80.4	9.4	153	4 US-09-366-887A-19	Sequence 19, Appl
23	76.8	9.0	360	2 US-08-479-126B-1	Sequence 1, Appl
24	76.8	9.0	360	2 US-08-726-830A-1	Sequence 1, Appl
25	76.8	9.0	360	3 US-08-995-156A-1	Sequence 1, Appl
26	76.8	9.0	360	3 US-09-044-856A-1	Sequence 1, Appl
27	76.8	9.0	360	3 US-09-044-855A-1	Sequence 1, Appl

28	76.8	9.0	360	4 US-09-419-281-1	Sequence 1, Appl
29	76.8	9.0	360	5 PCT-US94-05384-1	Sequence 1, Appl
30	76.8	9.0	360	5 PCT-US96-10087-1	Sequence 1, Appl
31	72.4	8.5	1235	3 US-08-808-720-8	Sequence 8, Appl
32	71.8	8.4	737	1 US-08-230-574-3	Sequence 3, Appl
33	68.6	8.0	99	3 US-07-927-391-12	Sequence 12, Appl
34	66	7.7	282	2 US-08-535-116-1	Sequence 1, Appl
35	61.6	7.2	87	3 US-07-927-391-11	Sequence 11, Appl
36	61.4	7.2	4256	3 US-08-995-156A-21	Sequence 21, Appl
37	61.4	7.2	4256	4 US-09-419-281-21	Sequence 21, Appl
38	61.2	7.1	285	3 US-08-995-156A-6	Sequence 6, Appl
39	61.2	7.1	285	4 US-09-419-281-6	Sequence 6, Appl
40	60.8	7.1	121	4 US-09-463-458A-4	Sequence 4, Appl
41	56.6	6.6	117	4 US-09-463-458A-3	Sequence 3, Appl
42	54.4	6.4	270	1 US-08-208-339A-3	Sequence 3, Appl
43	54.4	6.4	270	3 US-08-722-719-5	Sequence 5, Appl
44	53.8	6.3	1234	3 US-08-808-720-6	Sequence 6, Appl
45	53	6.2	800	1 US-08-230-574-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-07-927-391-15
; Sequence 15, Application US/07927391
; Patent No. 6001649
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: MILOUX, Brigitte
; APPLICANT: MINTY, Adrian
; APPLICANT: VIRA, Natalio
; TITLE OF INVENTION: Protein having a cytokin type
; TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
; TITLE OF INVENTION: for its preparation.
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: King Street Station, Suite 500, 1800 Diagonal
; STREET: Road, PO Box 299
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/927,391
; FILING DATE: 19920929
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 814 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 41..367

FEATURE:
NAME/KEY: mat_peptide
LOCATION: 140..367
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 41..139
US-07-927-391-15

Query Match 29.9%; Score 256; DB 3; Length 814;
Best Local Similarity 67.8%; Pred. No. 5.4e-53;
Matches 408; Conservative 0; Mismatches 180; Indels 14; Gaps 3;

QY 1 AACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCTCCAGATGAAGGTTCTGCA 60
DB 26 AAACCTCCAATTCTCATGTGGAAGCCCATGCCCCTCACCTCCACATGAAGGCTCTGCA 85
QY 61 GCGCTTCTGTGCTGCTGCTCATGCGAGCCACCTTTCAGCCCTCAGGACTTGTGCA 120
DB 86 GCACCTTCTGTGCTGCTGCTCACAGCAGCTGCTTTCAGCCCCCAGGGGCTTGTGCA 145
QY 121 GATTGAGTTTCCATTCATCACTGCTGCTTTAAGCTGATCAATAGAAATTCCTATC 180
DB 146 GTTGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 205
QY 181 CAGAGGCTGAGAGCTTACACAGAATCACCAACATCCATGTCCCAAGGAAGCTGTATC 240
DB 206 CAGAGGCTGAGAGCTTACAGAAAGAACACACAGTACCTGCTCCCGGAAGCTGTATC 265
QY 241 TTCAGAGCAAAACGGGCAAGAGGCTGTGCTGAGCCCAAGAGAGATGGTCAAGGAT 300
DB 266 TTCAGAGCAAAACGGGCAAGAGATCTGTGCTGAGCCCAAGAGAGATGGTCAAGGAT 325
QY 301 TCCATGAAGCATCTGAGCAAAATATTTCAAAATCTGAGCCCATGAGCCTTCATATGCA 360
DB 326 TTTATGAAGCAGCTGAGCAAAAGCAAACTCCAAAGCTTGAACATTCATGATGATA 385
QY 361 CTGA---GAGTCAGAGCTTGAAGAAAGCTTATTTTCCCAACCTCCCAAGGTC 416
DB 386 CTAAGAAAGCAAGCAGCTGAGCAAAAGCAAAATATTTGATTAACCTGCTTCAGAGT 445
QY 417 CAGTGTGACATTTATTTATTAACATCCACAAGA-GATTTATTTTAATTAATTAAG 475
DB 446 GGTCTGAGATTAATTTAATCTAATTTCTAAGGAATGAGCTTTATGTAATGTAAT 505
QY 476 CATATATTTCTTAATAAGTATTTATTTATTTAAGTGTGATGTTTAACTCTATCT 535
DB 506 CATGTTTCTTCTAGATTTTAA-----AAGTTAATTAATTTTAACTCTATCT 556
QY 536 GTCATATCTCTAGTGAATGTAATAATGCAAAATCTGATGTGTTTGTGTTTGTGTT 595
DB 557 TCCATGAGATTTTGTGGGTTTGAACATAAAGCCTGAGTATATGTCATCTCAGTGT 616
QY 596 TT 597
DB 617 GT 618

RESULT 2
US-09-366-887A-26
Sequence 26, Application US/09366887A
Patent No. 6403782
GENERAL INFORMATION:
APPLICANT: LUSTER, ANDREW D.
APPLICANT: LEDER, PHILIP
APPLICANT: ROTHENBERG, MARC
APPLICANT: GARCIA, EDUARDO
TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOKINE
FILE REFERENCE: 00383/025002
CURRENT APPLICATION NUMBER: US/09/366,887A
CURRENT FILING DATE: 1999-08-04
PRIOR APPLICATION NUMBER: 60/000,449
PRIOR FILING DATE: 1995-06-22
PRIOR APPLICATION NUMBER: 08/522,713

PRIOR FILING DATE: 1995-09-01
PRIOR APPLICATION NUMBER: 08/522,713
PRIOR FILING DATE: 1998-06-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for windows version 4.0
SEQ ID NO 26
LENGTH: 605
TYPE: DNA
ORGANISM: Mus musculus
US-09-366-887A-26

Query Match 27.2%; Score 233.2; DB 4; Length 605;
Best Local Similarity 69.4%; Pred. No. 1.5e-47;
Matches 379; Conservative 0; Mismatches 153; Indels 14; Gaps 4;

QY 1 AACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCTCCAGATGAAGGTTCTGCA 60
DB 31 AAACCAACACCTCTCAGCCAAAGCTCACACCTTCAGCTCCACATGAAGTCTCCGCA 90
QY 61 GCGCTTCTGTGCTGCTGCTCATGAGCCACTTTCAGCCCTCAGGACTTGTGCA 120
DB 91 GCACCTTCTGTGCTGCTGCTCATGAGCAGCTGCTTCAGCCCCCAGGGGCTGCGCA 150
QY 121 GATTGAGTTTCCATTCATCACTGCTGCTTTAAGCTGATCAATAGAAATTCCTATC 180
DB 151 GCTTCTG-----TCCCAACACCTGCTGCTTTAAGCTGCGCAATAGAAATACCCCTT 204
QY 181 CAGAGGCTGAGAGCTTACACAGAATCACCAACATCCATGTCCCAAGGAAGCTGTATC 240
DB 205 CAGGAGCTAGAGAGCTACAGAGATCACCAAGTGGCAATGTCCCAAGGAAGCTGTATC 264
QY 241 TTCAGAGCAAAACGGGCAAGAGGCTGTGCTGAGCCCAAGAGAGATGGTCAAGGAT 300
DB 265 TTCAGAGCAAAACGGGCAAGAGATCTGTGCTGAGCCCAAGAGAGATGGTCAAGGAT 324
QY 301 TCCATGAAGCATCTGAGCAAAATATTTCAAAATCTGAGCCCATGAGCCTTCA--TACATG 358
DB 325 TCCATGAAGTATCTGAGCAAAATATTTCAAAATCTGAGCCCATGAGCCTTCA--TACATG 384
QY 359 GACTGAGAGCTCAGAGCTTGAAGAAAGCTTATTTTCCCAACCTCCCAAGGTCGA 418
DB 385 GAAACCAACCAAGAGCCTGAGTGTGCTTAATTTGTTTC-----CCTTCTTCAATGCA 439
QY 419 GTGTGACATTTATTTATTAACATCCACAAGAGATTTATTTTAATTAATTAAGCAT 478
DB 440 TTTCTGAGGTAACTCATTAATCA-GTCCAAAGGAGATGGTTTATTAATTAATTAAT 498
QY 479 AATATTTCTTAATAAGTATTTAATTAATTTAAGTGTGATGTTTAACTCTATCTGTC 538
DB 499 TTTTCTTTTAAATAAAGATTTGATTTAATTTAATTTAAGGCTTTAAACTATGATC 558
QY 539 ATACAT 544
DB 559 CTCAT 564

RESULT 3
US-07-927-391-25
Sequence 25, Application US/07927391
Patent No. 6001649
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: MILOUX, Brigitte
APPLICANT: MINTY, Adrian
APPLICANT: VITTA, Natalio
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: for its preparation.
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal

STREET: Road, PO Box 299
 CITY: ALEXANDRIA
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/927,391
 FILING DATE: 19920929
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: SAXE, Bernhard D
 REGISTRATION NUMBER: 28,665
 REFERENCE/DOCKET NUMBER: 16781/369
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-9300
 TELEFAX: (703) 683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 741 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA

Query Match	25.78;	Score 219.8;	DB 3;	Length 741;
Best Local Similarity	68.18;	Pred. No. 2.9e-44;		
Matches 404; Conservative	0;	Mismatches 162;	Indels 27;	Gaps 65;

QY	1	AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAGATGAAGGTTTCTGCA	60
Db	26	AAAGATCCAATTCTCAAACTGAAGCTCGCACTCTCG - CCTCCAGCATGAAGTCTCTGCC	84
QY	61	GCGCTTCTGTGCTGCTGCTCATGCGAGCCACTTTCAGCCCTCAGGGACTGCTCAGCCA	120
Db	85	GCCCTTCTGTGCTGCTGCTCATAGAGCCACCTTCATTCCCAAGGGCTGCTCAGCCA	144
QY	121	GATTCAGTTTCCATTTCCAAATCACCTGCTGCTTAAAGTGATCAATAGAAATTCCTATC	180
Db	145	GATGCAATCATGATGCCCCAGTCACCTGCTGTATTAACTTCAACCAATAGAGACTCTCAGTG	204
QY	181	CAGAGGCTTGAGAGCTACACACAGAATCACCAACATCCCAATGTCCTCCAGAGAGCTGTGATC	240
Db	205	CAGAGGCTCGGAGCTATAGAGAATCACCAAGCAGCAAGTGTCCCAAGAGCTGTGATC	264
QY	241	TTCAAGACCAAAAGGGGCAAGAGGTGCTGCTGACCCCAAGAGAGATGGGTGAGGAT	300
Db	265	TTCAAGACCATTTGTGGCCAAGAGACTGTGCTGACCCCAAGCAGAGTGGGTTCAGGAT	324
QY	301	TCCATGAAGCATCTGGACCAAAATATTCAAAATCTGAAGCCATGAGCCTTCAATACATGGA	360
Db	325	TCCATGGAACACCTGGACAAAGCAAAACCAACTCCGAAGACTTGAACACACTCCACAA	384
QY	361	CTGAGAGCTCAGAGCTTGAAGAAAAGCTTATTATTTTTCCCAACCTCCCCAGGTGCAGT	420
Db	385	CCCA-----AGAATCTGCAGCTAA-----CTTATTTTCCCTAGCTTCCCCAGACACCT	435
QY	421	GTGACATTATTTTATTATTAACATCCACAAGAGATTATTTTAAATAATTAAAGCATAA	480
Db	436	GTTTATTATTATATAAT-----GAATTTGTTGTTGATGTGAACAT--	479
QY	481	TATTTCTAAAAAGTATTTAATTATATTTAAGTGTGATGTTTAACTCATCTGTCAT	540
Db	480	TATGCTTAAAGTAAATGTTAATCTTATTAAAGTATTGATGTTTAAAGTTTACTTTTCAT	539
QY	541	ACATCCTAGTGAATGTAAATGCAAAATCCTGGTGATGTTTTGTGTTTTG	593

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Db      540 GG-TACTAGTGTTTTATGATACAGAGACTTGGGGAATTCCTTCCCTTG 591
RESULT 4
5212073-1
; Patent No. 5212073
; APPLICANT: ROLLINS, BARRETT,STILES, CHARLES;WONG, GORDON G.
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/351,008
; FILING DATE:12-MAY-1989
; SEQ ID NO:1:
; LENGTH: 752
5212073-1

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Query Match	23.5%;	Score 201;	DB 6;	Length 752;
Best Local Similarity	77.28;	Pred. No. 1e-39;		
Matches 257; Conservative	0;	Mismatches 75;	Indels 1;	Gaps 11;

QY	1	AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCCAAGATGAAGGTTTCTGCA	60
Db	29	AAACATCCAAATTCTCAAACTGAAGCTCGCACTCTCG - CCTCCAGCATGAAGTCTCTGCC	87
QY	61	GGCCTTCTGTGCTGCTGCTCATATGAGCCACTTTACGCCCTCAGGACTTGCTCAGCCA	120
Db	88	GCCCTTCTGTGCTGCTGCTCATATGAGCCACTTCATTTCCCAAGGCTCGCTCAGCCA	147
QY	121	GATTCAGTTTCCATTTCCAATCACCTGCTTAAAGTGATCAATAGAAAATTCCTATC	180
Db	148	GATGCAATCAATGCCCCAGTCACCTGCTGCTATAACTTCACCAATAGGAAGATCTCAGTG	207
QY	181	CAGAGGCTGGAGAGCTACACACAGAATCACCAACATCCATGTCCCAAGAAAGCTGTGATC	240
Db	208	CAGAGGCTCGCGAGCTATAGAGAATCACCAAGCAAGTGTCCCAAGAAGCTGTGATC	267
QY	241	TTCAAGACCAAAACGGGGCAAGAGGTTGTGCTGACCCCCAAGAGAGATGGGTCAGGAT	300
Db	268	TTCAAGACCAATTGTGGCCAAAGGAGATGTGTGCTGACCCCCAAGCAGAAGTGGGTTGAGAT	327
QY	301	TCCATGAAGCATCTGGACCAAAATATTCAAAAT	333
Db	328	TCCATGGACCACTGGACAAGCAAAACCAAACT	360

RESULT 5
US-08-744-419-1

? sequence 1, application US/00/44419
 ? Patent No. 6274342
 ?
 ? GENERAL INFORMATION:
 ? APPLICANT: Gutierrez-Ramos et al.
 ? TITLE OF INVENTION: Monocyte Chemotactic Protein 5 (MCP-5) Molecules and
 ? NUMBER OF SEQUENCES: 10
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: LAHIVE & COCKFIELD
 ? STREET: 60 State Street, suite 510
 ? CITY: Boston
 ? STATE: Massachusetts
 ? COUNTRY: USA
 ? ZIP: 02109-1875
 ?
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: PatentIn Release #1.0, Version #1.25
 ?
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/744,419
 ?
 ? FILING DATE:
 ? CLASSIFICATION: 424
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: U.S. Provisional
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ?

```

; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIO-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..367
;
US-08-744-419-1

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Query Match	21.4%;	Score 183.6;	DB 4;	Length 540;
Best Local Similarity	69.7%;	Pred. No. 1.4e-35;		
Matches 340; Conservative	0;	Mismatches 129;	Indels 19;	Gaps 6;

QY	26	TCACACCCCTTGCCCTCCCAAGATGAGGTTCTGCGAGCGCTTCGTGCTGCTGCATCG	85
Db	36	TCGAAGTCTTTGACCTCAACATGAGATTTCACA ---CTTCTATGCCCTCCTCATAG	92
QY	86	CAGCCACTTTCAGCCCTCAGGACTTGCTCAGCCAGATTCAGTTCCATTCACCT	145
Db	93	CTACCACCATCAGTCCCTCAGGTATTGGCTGGACCAGATGCGGTGAGCACCCCACTCACGT	152
QY	146	GCTGCTTTAACGTGATCAATAGCAAAATTCCTATCCAGAGGCTGGAGAGCTACACAAGA	205
Db	153	GCTGTTATAATGTTGTTAAGCAGAGATTCACTGCCGAAGCTGAAGAGCTACAGGAGAA	212
QY	206	TCACCAACATCCAATGTCCCAAGAGAGCTGTGATCTTCAAGACCAACGGGSCAAGGAG	265
Db	213	TCACAAGCAGCCAGTGTCCCGGGAAGCTGTGATCTTCAGGACCATCTGATTAAGGAGA	272
QY	266	TCTGTGCTGACCCCAAGAGAGATGGGTCAGGATTCATGAAGCATCTGACCAATAT	325
Db	273	TCTGTGCTGACCCCAAGAGAGATGGGTTAAGAATTCCATAAACCACTGGATTAAGACGT	332
QY	326	TTCAAAATCTGAGGCCATGAGCCTTCATACATGGAGCTGAGAGCTCAGAGCTTGACAAG	385
Db	333	CTC-AAACCTTCATCCTTGAACCTTCATGTCTAGGCTGAGAGT ----TCCAAAACTC	385
QY	386	CTTATTTATTTTCCCAACCTCCCCAGGTCAGTGTGACATTAATTTATTAACATCC	445
Db	386	TTACGTATTTCCCCCTGAAGTTCGCCACGGGCAGGGTGATA ---TTTATTAATGATATCT	441
QY	446	ACAAAGAGATTATTTTAAATTAATTAAGCATATAATTTCTTAAAAAGATTTAATAT	505
Db	442	AAAAAGAGAT - GTTTTAAATAATTTAA ---ACAAACTTGCTTAAATAATTAATGCT	496
QY	506	ATTTAAGT 513	
Db	497	ATTTAAGT 504	

RESULT 6
 US-08-613-822-3
 ; Sequence 3, Application US/08613822
 ; Patent No. 6174995
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Haodong
 ; TITLE OF INVENTION: Human Chemokine Polypeptides
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: USA

```

1 ZIP: 20850
2
3 COMPUTER READABLE FORM:
4
5 MEDIUM TYPE: Floppy disk
6
7 COMPUTER: IBM PC compatible
8
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10
11 SOFTWARE: PatentIn Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/08/613,822
16
17 FILING DATE: 23-FEB-1996
18
19 CLASSIFICATION: 435
20
21 ATTORNEY/AGENT INFORMATION:
22
23 NAME: Millstein, Larry S
24
25 REGISTRATION NUMBER: 34,679
26
27 TELECOMMUNICATION INFORMATION:
28
29 TELEPHONE: 301-309-8504
30
31 TELEFAX: 301-309-8512
32
33 INFORMATION FOR SEQ ID NO: 3:
34
35 SEQUENCE CHARACTERISTICS:
36
37 LENGTH: 297 base pairs
38
39 TYPE: nucleic acid
40
41 STRANDEDNESS: single
42
43 TOPOLOGY: linear
44
45 MOLECULE TYPE: DNA (genomic)
46
47 FEATURE:
48
49 NAME/KEY: CDS
50
51 LOCATION: 1..294
52
53 US-08-613-822-3

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Query Match	19.98;	Score 170.4;	DB 4;	Length 297;
Best Local Similarity	75.38;	Pred. No. 1.7e-32;		
Matches 226; Conservative	0;	Mismatches 71;	Indels 3;	Caps 1;

QY		46	ATGAAGGTTTCTGCAGCGCCTTCTGTGCCCTGCTGCTCATGGCAGCCACTTTACGCCCTCAG	103
Db		1	ATGAAAGTTTCTGCAGTGCTTCTGTGCCCTGCTGCTCATGACAGCAGCTTTCAACCCCCAG	60
QY		106	GGACTTGCTCAGCCAGATTTCAGTTTCCATTCCAATCACCTGCTGCTTTAAGTGATCAAT	165
Db		61	GGACTTGCTCAGCCAGATGCACATCAACGTCCCATCTACTTGCTGCTTCACATTTAGCAGT	120
QY		166	AGGAAAATTCCTATPCCAGAGGCTGGAGAGCTACACAAGAATCACCAACATCCATGTC	225
Db		121	AAGAAGATCTCCTTGACAGAGGCTGAAGAGCTA---TGTGATCACACCACAGCAGGTGTCCC	177
QY		226	AAGGAAGCTGTGATCTTCAAGACCAACAACGGGGCAAGAGGTCTGTGCTGACCCCAAGGAG	285
Db		178	CAGAAGGCTGTCACTCTTCAAGAACCAAACTGGGGCAAGAGATCTGTGCTGACCCCAAAGGAG	237
QY		286	AGATGGGTCAGGGATTCATGAAAGCATCTGGACCAATAATTTCAAAAATCTGAAGCCATGA	345
Db		238	AAGTGGGTCAGAAATTATATGAACAACCTGGGGCCGGAAGCTCACACCCTGAAGACTTGA	297

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RESULT 7
US-08-852-212-1
; Sequence 1, Application US/08852212
; Patent No. 6290948
; GENERAL INFORMATION:
; APPLICANT: White et al.
; TITLE OF INVENTION: Method of Treating Sepsis and ARDS using Chemokine Beta-10
; FILE REFERENCE: PF501
; CURRENT APPLICATION NUMBER: US/08/852,212
; CURRENT FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: 60/017,871
; EARLIER FILING DATE: 1996-05-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
;

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; LOCATION: (1)..(297)
US-08-852-212-1
Query Match          19.9%; Score 170.4; DB 4; Length 297;
Best Local Similarity 75.3%; Pred. No. 1.7e-32;
Matches 226; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 46 ATGAAGTTTCTGACGCGCTTCTGCTGCTGCTCATGGCAGCCACTTTCAGCCCTCAG 105
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATGAAGTTTCTGACAGTGTCTGTGCTGCTGCTCATGACAGCAGCTTTCACCCCCAG 60

QY 106 GGACTTGCTCAGCCAGATTTCAGTTTCCATTCACCTGCTGCTTAAAGTGATCAAT 165
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GGACTTGCTCAGCCAGATTTCAGTTTCCATTCACCTGCTGCTTAAAGTGATCAAT 120

QY 166 AGGAAATTCCTATCCAGAGGCTGGAGAGCTACACAGAATCACCAACATCCATGCC 225
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 AAGAGATCTCTTGCAGAGGCTGAAGAGCTA--TGTGATCACCAAGGAGTGTCCC 177

QY 226 AAGGAGCTGTGATCTTCAAGACCAAAAGGGGCAAGAGGCTGTGCTGACCCCAAGAG 285
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 CAGAGGCTGTGATCTTCAAGACCAAAAGGGGCAAGAGATCTGTGCTGACCCCAAGAG 237

QY 286 AGATGGGTGAGGATTCATTCAGAACCAATCTGACCAATATTTCAAAATCTGAAGCCATGA 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 AAGTGGGTCCAGAAATATATGAACACCTGGGCCGGAAGCTCACACCTGAAGACTTGA 297
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```

RESULT 8
US-09-479-729B-3
; Sequence 3, Application US/09479729B
; Patent No. 6391589
; GENERAL INFORMATION:
; APPLICANT: Olsen, et al
; TITLE OF INVENTION: Human Chemokine Beta-10 Mutant Polypeptides
; FILE REFERENCE: PF504
; CURRENT APPLICATION NUMBER: US/09/479,729B
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: PCT/US94/09484
; PRIOR FILING DATE: 1994-08-23
; PRIOR APPLICATION NUMBER: 08/458,355
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 08/462,967
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 60/115,439
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(294)
US-09-479-729B-3
```

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Query Match          19.9%; Score 170.4; DB 4; Length 297;
Best Local Similarity 75.3%; Pred. No. 1.7e-32;
Matches 226; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 46 ATGAAGTTTCTGACGCGCTTCTGCTGCTGCTCATGGCAGCCACTTTCAGCCCTCAG 105
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATGAAGTTTCTGACAGTGTCTGTGCTGCTGCTCATGACAGCAGCTTTCACCCCCAG 60

QY 106 GGACTTGCTCAGCCAGATTTCAGTTTCCATTCACCTGCTGCTTAAAGTGATCAAT 165
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GGACTTGCTCAGCCAGATTTCAGTTTCCATTCACCTGCTGCTTAAAGTGATCAAT 120

QY 166 AGGAAATTCCTATCCAGAGGCTGGAGAGCTACACAGAATCACCAACATCCATGCC 225
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 AAGAGATCTCTTGCAGAGGCTGAAGAGCTA--TGTGATCACCAAGGAGTGTCCC 177
```

```

QY 226 AAGGAGCTGTGATCTTCAAGACCAAAAGGGGCAAGAGGCTGTGCTGACCCCAAGAG 285
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 CAGAGGCTGTGATCTTCAAGACCAAAAGGGGCAAGAGATCTGTGCTGACCCCAAGAG 237

QY 286 AGATGGGTGAGGATTCATTCAGAGCATCTGAGACCAATATTTCAAAATCTGAAGCCATGA 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 AAGTGGGTCCAGAAATATATGAACACCTGGGCCGGAAGCTCACACCTGAAGACTTGA 297
```

```

RESULT 9
US-09-261-201A-3
; Sequence 3, Application US/09261201A
; Patent No. 6458349
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Polynucleotides Encoding Chemokine B-4
; FILE REFERENCE: PF132P1D1
; CURRENT APPLICATION NUMBER: US/09/261,201A
; CURRENT FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: 08/458,355
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/US94/09484
; PRIOR FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(294)
; OTHER INFORMATION:
US-09-261-201A-3
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Query Match          19.9%; Score 170.4; DB 4; Length 297;
Best Local Similarity 75.3%; Pred. No. 1.7e-32;
Matches 226; Conservative 0; Mismatches 71; Indels 3; Gaps 1;
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QY 46 ATGAAGTTTCTGACGCGCTTCTGCTGCTGCTCATGGCAGCCACTTTCAGCCCTCAG 105
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATGAAGTTTCTGACAGTGTCTGTGCTGCTGCTCATGACAGCAGCTTTCACCCCCAG 60

QY 106 GGACTTGCTCAGCCAGATTTCAGTTTCCATTCACCTGCTGCTTAAAGTGATCAAT 165
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GGACTTGCTCAGCCAGATTTCAGTTTCCATTCACCTGCTGCTTAAAGTGATCAAT 120

QY 166 AGGAAATTCCTATCCAGAGGCTGGAGAGCTACACAGAATCACCAACATCCATGCC 225
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Db 121 AAGAGATCTCTTGCAGAGGCTGAAGAGCTA--TGTGATCACCAAGGAGTGTCCC 177

QY 226 AAGGAGCTGTGATCTTCAAGACCAAAAGGGGCAAGAGGCTGTGCTGACCCCAAGAG 285
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 CAGAGGCTGTGATCTTCAAGACCAAAAGGGGCAAGAGATCTGTGCTGACCCCAAGAG 237

QY 286 AGATGGGTGAGGATTCATTCAGAGCATCTGAGACCAATATTTCAAAATCTGAAGCCATGA 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 AAGTGGGTCCAGAAATATATGAACACCTGGGCCGGAAGCTCACACCTGAAGACTTGA 297
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RESULT 10
US-08-744-419-3
; Sequence 3, Application US/08744419
; Patent No. 6274342
; GENERAL INFORMATION:
; APPLICANT: Gutierrez-Ramos et al.
; TITLE OF INVENTION: Monocyte Chemotactic Protein 5 (MCP-5) Molecules
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
```

```

: COUNTRY: USA
: ZIP: 02109-1875
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/744,419
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: U.S. Provisional
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Arnold, Beth E.
: REGISTRATION NUMBER: 35,430
: REFERENCE/DOCKET NUMBER: MIQ-008
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)227-5941
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 315 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
US-08-744-419-3
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Query Match	19.18;	Score 163.2;	DB 4;	Length 315;
Best Local Similarity	72.7%;	Pred. No. 9.7e-31;		
Matches 224; Conservative	0;	Mismatches 83;	Indels 1;	Gaps 1;

[illegible]

RESULT 11
US-09-366-887A-5
; Sequence 5, Application US/09366887A
; Patent No. 6403782
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/366, 887A
; CURRENT FILING DATE: 1999-08-04
; PRIORITY APPLICATION NUMBER: 60/000,449

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: PRIOR FILING DATE: 1995-06-22
: PRIOR APPLICATION NUMBER: 08/522,713
: PRIOR FILING DATE: 1995-09-01
: PRIOR APPLICATION NUMBER: 08/522,713
: PRIOR FILING DATE: 1998-06-16
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 994
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (35)...(325)
US-09-366-887A-5

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Query Match	18.3%;	Score 156.8;	DB 4;	Length 994;
Best Local Similarity	69.9%;	Pred. No. 5.3e-29;		
Matches 228; Conservative	0;	Mismatches 92;	Indels 6;	Gaps 1;

OY	22	AAGCTCACACCCCTTGCCCCCTCCAAGAATGAAGTTTCTGTGCAGCGGCTTCGTGGCCTGGCTGTC	81
Db	11	AACTTCCATCTGTCTCCCTCCACCATTGCAGAGCTCCACAGCGGCTTCTAATTCCTGTGCTGTC	70
OY	82	ATGGCAGCCACTTTCAGCCCCTCAGGCACTTGCTCAGCCAGATTTCAGTTTCCATTCCAATC	141
Db	71	ACGGTCACTTCCTTCACTCCAGGCTGCCGCTCACCAGGC-----TCCATCCCAACT	124
OY	142	ACCTGCTGCTTTAACGTGATCAATAAGAAAATTCTTATCCAGAGCGCTGGAGAGCTACACA	201
Db	125	T CCTGCTGCTTTATCATGACACAGTAGAGATCCCAACACACACTACTGAAGAGCTACAAA	184
OY	202	AGAATCACCAACATCCCAATGTCCCAAGGAAGCTGTGATCTTCAAGACCAAACGGGGCAAG	261
Db	185	AGAATCACCAACAACAGATGACACCTGGAAGCCATAGTCTTCAAGACCAGGTGGGCAAA	244
OY	262	GAGGTCTGTGCTGACCCCAAGAGAGATGGGT CAGGGATTCCATGAAGCATCTGGACCAA	321
Db	245	GAGATCTGTGCTGACCCCAAGAGAGATGGGT CCAGGATGCCACAAAGCACTTGACC AA	304
OY	322	ATATTTCAAATCTGAAGCCATGAGC	347
Db	305	AAACTCCAAACTCCAAAAACCATTAAC	330

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RESULT 12
US-09-366-887A-15
; Sequence 15, Application US/09366887A
; Patent No. 6403782
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC.
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/366, 887A
; CURRENT FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449
; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Guinea pig
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(356)

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; REFERENCE/DOCKET NUMBER: 16781/369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
US-07-927-391-13

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Query Match 16.1%; Score 138; DB 3; Length 228;
Best Local Similarity 75.7%; Pred. No. 1e-24;
Matches 171; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY	115	CAGCCAGATTCAGTTTCCATTCACATCACCTGCTGCTTTAACGTGATCAATGCAAAATT	174
Db	1	CAGCCAGTTGGATTAACTTAACCTCACTACCTGCTCTACAGATTTATCAATAGAAATC	60
QY	175	CCTATCCAGAGGCTGGAGAGCTACACAGAATCACCAACATCCATGTCCCAAGSAGCT	234
Db	61	CCTAAGCAGAGGCTGGAGAGCTACAGAGGAGCAACCAAGTAGCCACTGTCCCCGGGAGCT	120
QY	235	GTGATCTTCAAGACCAACCGGGCAGAGGCTCTGTGCTGACCCCAAGGAGAGATGGGTC	294
Db	121	GTAATCTTCAAGACCAAACTGGACAGAGATCTGTGCTGACCCCAACAGAGATGGGTC	180
QY	295	AGGATTCATGAAGCATCTGGACCAAAATATTTCAAAATCTGAAGC	340
Db	181	CAGGACTTTATGAAGCACCTGGACAGAAACCCTCAAACTCCAAAGC	226

RESULT 15
US-08-250-958-3
; Sequence 3, Application US/08250958

GENERAL INFORMATION:
APPLICANT: LYLE, LEON R.
APPLICANT: KUNKEL, STEVEN L.
APPLICANT: STRIETER, ROBERT M.
TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING
TITLE OF INVENTION: VASCULAR RESTENOSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,958
FILING DATE: 27-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,678
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: WALKER, Barbara W.
REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 2077-206A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031

```

; INFORMATION FOR SEQ ID NO: 3;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
;
US-08-250-958-3

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Query Match	16.1%;	Score 137.4;	DB 1;	Length 228;
Best Local Similarity	61.2%;	Pred. No. 1.5e-24;		
Matches 139;	Conservative 32;	Mismatches 56;	Indels 0;	Gaps 0;

QY	115	CAGCCAGATTCAAGTTTCCATTCACATCACCTGCTGCTTTAACGTGATCAATAGGAAATT	174
		: : : : : : : :	
Db	1	CAGCCAGAUCCAUAUCAAUGCCCCAGUCACCUUGUUAUACUUCACCAUAUAGGAAGAU	60
QY	175	CCTATCCAGAGGCTGAGAGCTACACAAGATCACCAACATCCATGTGCCAAGGAAGCT	234
		: : : : : :	
Db	61	UCAGUGCAGAGGCUCCGAGAGCUAUAAGAUAUACCAAGCAGCAAGUGUCCCAAGAAGACU	120
QY	235	GTGATCTTCAGACCAACGGGGCAGGAGGTCTGTGCTGACCCCAAGAGAGATGGGTC	294
		: : : : :	
Db	121	GUGAUCUUCAGACCAUUGUGGCCAAGAGAUGUGUGUGACCCCAAGCAGAGAUGGGCU	180
QY	295	AGGATTCATGAAGCATCTGACCAATAATTTCAAAATCTGAAGCC	341
		: : :	
Db	181	CAGGAUCCCAUGCACCACCUUGAGCAAGCAAAACCCAAACUCCGAAGAC	227

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Search completed: February 18, 2003, 01:57:48
Job time : 63 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 03:06:42 ; Search time 70 Seconds
(without alignments)
6228.301 Million cell updates/sec

Title: US-10-033-067-2
Perfect score: 856
Sequence: 1 aaacctcacctctcatgct.....actaaaaaaaaaaaaaa 856

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 424239 segs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	849	99.2	856	US-10-033-067-2	Sequence 2, Appli
2	842.2	98.4	870	US-10-044-090-581	Sequence 581, App
3	841	98.2	2738	US-08-927-939-80	Sequence 80, Appl
4	257.6	30.1	1085	US-08-927-939-81	Sequence 81, Appl
5	244	28.5	256	US-10-033-067-7	Sequence 7, Appli
6	237	27.7	839	US-08-927-939-51	Sequence 51, Appl
7	235.6	27.5	817	US-10-044-090-837	Sequence 837, App
8	230.8	27.0	987	US-10-044-090-494	Sequence 494, App
9	227.8	26.6	685	US-08-927-939-76	Sequence 76, Appl
10	222.6	26.0	1712	US-09-981-876-106	Sequence 106, App
11	222.6	26.0	1712	US-09-148-545-106	Sequence 106, App
12	222.6	26.0	1822	US-09-981-876-105	Sequence 105, App
13	222.6	26.0	1822	US-09-148-545-105	Sequence 105, App
14	221.4	25.9	804	US-10-044-090-583	Sequence 583, App
15	218.8	25.6	600	US-10-044-090-822	Sequence 822, App
16	216.4	25.3	383	US-10-114-893-51	Sequence 51, Appl
17	213	24.9	236	US-10-033-067-5	Sequence 5, Appli
18	204	23.8	647	US-09-777-430A-72	Sequence 72, Appl
19	203	23.7	825	US-08-927-939-28	Sequence 28, Appl

20	203	23.7	825	8	US-08-927-939-33	Sequence 33, Appl
21	203	23.7	832	12	US-10-044-090-838	Sequence 838, App
22	203	23.7	860	10	US-09-872-611A-3	Sequence 3, Appli
23	199.4	23.3	228	9	US-10-033-067-6	Sequence 6, Appli
24	194	22.7	338	9	US-10-040-739-793	Sequence 793, App
25	183.4	21.4	289	9	US-10-057-275-1	Sequence 1, Appli
26	170.4	19.9	297	9	US-10-164-621-3	Sequence 3, Appli
27	170.4	19.9	297	9	US-10-125-451-3	Sequence 3, Appli
28	168.8	19.7	297	10	US-09-872-611A-1	Sequence 1, Appli
29	154.8	18.1	258	9	US-09-796-692-7869	Sequence 7869, Ap
30	149.2	17.4	972	9	US-09-792-793A-61	Sequence 61, Appl
31	149.2	17.4	978	9	US-09-792-793A-62	Sequence 62, Appl
32	149.2	17.4	993	9	US-09-792-793A-63	Sequence 63, Appl
33	139	16.2	978	9	US-09-792-793A-52	Sequence 52, Appl
34	139	16.2	984	9	US-09-792-793A-53	Sequence 53, Appl
35	139	16.2	999	9	US-09-792-793A-54	Sequence 54, Appl
36	119.2	13.9	253	10	US-09-833-381-1229	Sequence 1229, Ap
37	110.4	12.9	453	10	US-09-864-761-1789	Sequence 1789, Ap
38	104.4	12.2	476	10	US-09-864-761-5570	Sequence 5570, Ap
39	102.2	11.9	400	10	US-09-833-381-1234	Sequence 1234, Ap
40	99.8	11.7	724	12	US-10-044-090-839	Sequence 839, App
41	93.8	11.0	231	9	US-09-792-793A-67	Sequence 67, Appl
42	93.8	11.0	978	9	US-09-792-793A-55	Sequence 55, Appl
43	93.8	11.0	984	9	US-09-792-793A-56	Sequence 56, Appl
44	93.8	11.0	999	9	US-09-792-793A-57	Sequence 57, Appl
45	79.6	9.3	360	10	US-09-864-761-5454	Sequence 5454, Ap

ALIGNMENTS

RESULT 1
US-10-033-067-2
Sequence 2, Application US/10033067
Patent No. US20020164704A1
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROTEIN
FILE REFERENCE: PF-0069-1 CON
CURRENT APPLICATION NUMBER: US/10/033,067
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 08/683,655
PRIOR FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 856
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID No. US20020164704A1 965517CB1
NAME/KEY: unsure
LOCATION: 628, 650, 653, 676, 769, 779, 820
OTHER INFORMATION: a, t, c, g, or other
US-10-033-067-2

Query Match 99.2%; Score 849; DB 9; Length 856;
Best local Similarity 100.0%; Pred. No. 1.9e-147;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAACCTTCACCTCTCATGCTGAAGCTCACACCTTGCCCTCCAAGATGAAGTTTCTGCA	60
DB	1	AAACCTTCACCTCTCATGCTGAAGCTCACACCTTGCCCTCCAAGATGAAGTTTCTGCA	60
QY	61	GGCGTTCTGTCCTGCTGCTCATGGCAGCAGCTTTCAGCCCTCAGGACTGCTCAGCCA	120
DB	61	GGCGTTCTGTCCTGCTGCTCATGGCAGCAGCAGCTTTCAGCCCTCAGGACTGCTCAGCCA	120
QY	121	GATTCAGTTTCCATTCACATCACCTGCTGCTTAAAGTGATCAATAGAAATTCCTATC	180

Db 121 GATTTCAGTTTCCATTCCAAATCACCCTGCTGCTTTAACCTGATCAATAGCAAAATPCCATTTC
QY 181 CAGAGGCTGGAGAGCTACACAGAATCACCACATCCAAATGTCCTCAAGAGCTGTGATC 240
Db 181 CAGAGGCTGGAGAGCTACACAGAATCACCACATCCAAATGTCCTCAAGAGCTGTGATC 240
QY 241 TTCAGAGCCAAACGGGGCAAGAGAGTCTGTGCTGACCCCAAGAGAGATGGGTGACGGAT 300
Db 241 TTCAGAGCCAAACGGGGCAAGAGAGTCTGTGCTGACCCCAAGAGAGATGGGTGACGGAT 300
QY 301 TCCATGAGCATCTGGACCAAAATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 360
Db 301 TCCATGAGCATCTGGACCAAAATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 360
QY 361 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTATTTCCTCCCAAGCTCCCAAGGTGACGT 420
Db 361 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTATTTCCTCCCAAGCTCCCAAGGTGACGT 420
QY 421 GTGACATTTATTTATTAACATCCACAAAGAGATTATTTTAAATAATTAAAGCATAA 480
Db 421 GTGACATTTATTTATTAACATCCACAAAGAGATTATTTTAAATAATTAAAGCATAA 480
QY 481 TATTTCTTAAAGATATTTAATTAATTTAAGTTGTGATGTTTAACTCTATCTGTCAT 540
Db 481 TATTTCTTAAAGATATTTAATTAATTTAAGTTGTGATGTTTAACTCTATCTGTCAT 540
QY 541 ACATCTAGTGAATGTAAATGCAAAATCCTGTGATGTTTGTGTTTGTTCCT 600
Db 541 ACATCTAGTGAATGTAAATGCAAAATCCTGTGATGTTTGTGTTTGTTCCT 600
QY 601 GTGAGCTCAACTAAGTTCACGGCCAAANGTCATTTCTCCCTACACNGTNGTAGTG 660
Db 601 GTGAGCTCAACTAAGTTCACGGCCAAANGTCATTTCTCCCTACACNGTNGTAGTG 660
QY 661 TTGTGGGGTCTCCCTNGATGATCAAGGTGAACACTAGGTATCTTTGGCAATCAGT 720
Db 661 TTGTGGGGTCTCCCTNGATGATCAAGGTGAACACTAGGTATCTTTGGCAATCAGT 720
QY 721 GCTCTGTAAGTCAAAATGTGCTTTTGTACTGCTGTGTTGAAATTTGANGTACTGTANA 780
Db 721 GCTCTGTAAGTCAAAATGTGCTTTTGTACTGCTGTGTTGAAATTTGANGTACTGTANA 780
QY 781 TAACTATGGAATTTGAAAAAAATTTCAAAAAAGAAAAANATATATATTAAATACTA 840
Db 781 TAACTATGGAATTTGAAAAAAATTTCAAAAAAGAAAAANATATATATTAAATACTA 840
QY 841 AAAAAAAAAAAAAAAA 856
Db 841 AAAAAAAAAAAAAAAA 856

RESULT 2
US-10-044-090-581
; Sequence 581, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044, 090
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 581
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 2883526CB1
US-10-044-090-581

Query Match 98.4%; Score 842.2; DB 12; Length 870;

Best Local Similarity 98.8%; Pred. No. 3.3e-146;
Matches 844; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAAGATGAGGTTTCTGCA 60
Db 17 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAAGATGAGGTTTCTGCA 76
QY 61 GCGCTTCGTGCTGCTGCTCATGGCAGCCATTTCAGCCCTCAGGGACTGCTCAGCCA 120
Db 77 GCGCTTCGTGCTGCTGCTCATGGCAGCCATTTCAGCCCTCAGGGACTGCTCAGCCA 136
QY 121 GATTTCAGTTTCCATTCCAAATCACCCTGCTGCTTTAACGTGATCAATAGGAAATTCCTATC 180
Db 137 GATTTCAGTTTCCATTCCAAATCACCCTGCTGCTTTAACGTGATCAATAGGAAATTCCTATC 196
QY 181 CAGAGGCTGGAGAGCTACACAGAATCACCACATCCCAATGTCCCAAGAGAGCTGTGATC 240
Db 197 CAGAGGCTGGAGAGCTACACAGAATCACCACATCCCAATGTCCCAAGAGAGCTGTGATC 256
QY 241 TTCAGAGCCAAACGGGGCAAGAGAGTCTGTGCTGACCCCAAGAGAGAGATGGGTGACGGAT 300
Db 257 TTCAGAGCCAAACGGGGCAAGAGAGTCTGTGCTGACCCCAAGAGAGAGATGGGTGACGGAT 316
QY 301 TCCATGAGCATCTGGACCAAAATTTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 360
Db 317 TCCATGAGCATCTGGACCAAAATTTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 376
QY 361 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTATTTCCTCCCAAGCTCCCAAGGTGACGT 420
Db 377 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTATTTCCTCCCAAGCTCCCAAGGTGACGT 436
QY 421 GTGACATTTATTTATTAACATCCACAAAGAGATTATTTTAAATAATTAAAGCATAA 480
Db 437 GTGACATTTATTTATTAACATCCACAAAGAGATTATTTTAAATAATTAAAGCATAA 496
QY 481 TATTTCTTAAAGATATTTAATTAATTTAAGTTGTGATGTTTAACTCTATCTGTCAT 540
Db 497 TATTTCTTAAAGATATTTAATTAATTTAAGTTGTGATGTTTAACTCTATCTGTCAT 556
QY 541 ACATCTAGTGAATGTAAATGCAAAATCCTGTGATGTTTGTGTTTGTTCCT 600
Db 557 ACATCTAGTGAATGTAAATGCAAAATCCTGTGATGTTTGTGTTTGTTCCT 616
QY 601 GTGAGCTCAACTAAGTTCACGGCCAAANGTCATTTCTCCCTCCTACACNGTNGTAGTG 660
Db 617 GTGAGCTCAACTAAGTTCACGGCCAAANGTCATTTCTCCCTCCTACCTGCTGAGTG 676
QY 661 TTGTGGGGTCTCCCTNGATGATCAAGGTGAACACTAGGTATCTTTGGCAATCAGT 720
Db 677 TTGTGGGGTCTCCCTNGATGATCAAGGTGAACACTTTGGTATTTCTTTGGCAATCAGT 736
QY 721 GCTCTGTAAGTCAAAATGTGCTTTTGTACTGCTGTGTTGAAATTTGANGTACTGTANA 780
Db 737 GCTCTGTAAGTCAAAATGTGCTTTTGTACTGCTGTGTTGAAATTTGANGTACTGTANA 796
QY 781 TAACTATGGAATTTGAAAAAAATTTCAAAAAAGAAAAANATATATATTAAATACTA 840
Db 797 TAACTATGGAATTTGAAAAAAATTTCAAAAAAGAAAAANATATATATTAAATACTA 856
QY 841 AAAAAAAAAAAAAAAA 854
Db 857 AAAAAAAAAAAAAAAA 870

RESULT 3
US-08-927-939-80
; Sequence 80, Application US/08927939
; Patent No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Granger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; augment an inflammatory response.

FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 2738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (123)...(353)
US-08-927-939-80

Query Match 98.2%; Score 841; DB 8; Length 2738;
Best Local Similarity 98.6%; Pred. No. 7e-146;
Matches 844; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCCCAAGATGAAGTTCTGCA 60
Db 12 AACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCCCAAGATGAAGTTCTGCA 71
QY 61 GCGCTTCTGTGCTGCTGCTCATGCGCAGCCACTTTCAGCCCTCAGGGACTGCTCAGCCA 120
Db 72 GCGCTTCTGTGCTGCTGCTCATGCGCAGCCACTTTCAGCCCTCAGGGACTGCTCAGCCA 131
QY 121 GATTCAGTTTCCATTCCAAATCACCCTGCTGCTTTAACGTGATCAATAGGAAATTCCTATC 180
Db 132 GATTCAGTTTCCATTCCAAATCACCCTGCTGCTTTAACGTGATCAATAGGAAATTCCTATC 191
QY 181 CAGAGGCTGGAGAGCTACACAGAATCACCAACATCCCAATGTCCCAAGGAAGCTGTGATC 240
Db 192 CAGAGGCTGGAGAGCTACACAGAATCACCAACATCCCAATGTCCCAAGGAAGCTGTGATC 251
QY 241 TTCAAGACCAACGCGGCAAGAGGTCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT 300
Db 252 TTCAAGACCAACGCGGCAAGAGGTCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT 311
QY 301 TCCATGAAGCATCTGGAGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 360
Db 312 TCCATGAAGCATCTGGAGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 371
QY 361 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTTTCCCAACCTCCCCAGGTGCAGT 420
Db 372 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTTTCCCAACCTCCCCAGGTGCAGT 431
QY 421 GTGACATTTATTTATATACATCCACAAGAGATTTTAAATTAATTTAAAGCATAA 480
Db 432 GTGACATTTATTTATATATACATCCACAAGAGATTTTAAATTAATTTAAAGCATAA 491
QY 481 TATTTCTTAAAAAGTATTTAATTAATTTAAGTTGTTGATGTTTAACTCTATCTGCAT 540
Db 492 TATTTCTTAAAAAGTATTTAATTAATTTAAGTTGTTGATGTTTAACTCTATCTGCAT 551
QY 541 ACATCCTAGTGAATGTAAATGCAAAATCCTGGTGATGTGTTTGTGTTTGTTCCT 600
Db 552 ACATCCTAGTGAATGTAAATGCAAAATCCTGGTGATGTGTTTGTGTTTGTTCCT 611
QY 601 GTGAGCTCAACTAAGTTCACGCGCAANGTCATTTCTCCCTCCTACCNCTAGTAGTG 660
Db 612 GTGAGCTCAACTAAGTTCACGCGCAAAATGTCATTTCTCCCTCCTACCTGTCGTAGTG 671
QY 661 TTGTGGGGTCTCCCNCTGATCATCAAGGTGAAGACCTTAGGTATCTTTGGCAATCAGT 720
Db 672 TTGTGGGGTCTCCCATGGATCATCAAGGTGAAGACCTTAGGTATCTTTGGCAATCAGT 731
QY 721 GCTCCTGTAAAGTCAAAATGTGTGCTTTGTAAGTGTGTTGAATGANGTACTGTANA 780
Db 732 GCTCCTGTAAAGTCAAAATGTGTGCTTTGTAAGTGTGTTGAATGANGTACTGTANA 791
QY 781 TAACTATGAATTTTGAAGAAAAAATTTCAAGAAAAAANATATATATTAATTTAAACTA 840
Db 792 TAACTATGAATTTTGAAGAAAAAATTTCAAGAAAAAANATATATATTAATTTAAACTA 851

QY 841 AAAAAAAAAAAAAA 856
Db 852 AAAAAAAAAAAAAA 867

RESULT 4

US-08-927-939-81
; Sequence 81, Application US/08927939
; Patent No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Granger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 1085
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (329)...(625)
US-08-927-939-81

Query Match 30.1%; Score 257.6; DB 8; Length 1085;
Best Local Similarity 67.9%; Pred. No. 6.8e-39;
Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;

QY 1 AACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCAAGATGAAGTTTCTGCA 60
Db 284 AACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCAAGATGAAGTTTCTGCA 343
QY 61 GCGCTTCTGTGCTGCTGCTCATGCGCAGCCACTTTCAGCCCTCAGGAGCTGCTCAGCCA 120
Db 344 GCACTTCTGTGCTGCTGCTCATGCGCAGCCACTTTCAGCCCTCAGGAGCTGCTCAGCCA 403
QY 121 GATTCAGTTTCCATTCCAAATCACCCTGCTGCTTTAACGTGATCAATAGGAAATTCCTATC 180
Db 404 GTTGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 463
QY 181 CAGAGGCTGGAGAGCTACACAAGAAATCACCAATCCCAATGTCCCAAGGAAGCTGTGATC 240
Db 464 CAGAGGCTGGAGAGCTACACAAGAAATCACCAATCCCAATGTCCCAAGGAAGCTGTGATC 523
QY 241 TTCAAGACCAACGCGGCAAGAGGTCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT 300
Db 524 TTCAAGACCAACGCGGCAAGAGATCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT 583
QY 301 TCCATGAAGCATCTGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 360
Db 584 TTTATGAAGCATCTGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 643
QY 361 CTGAG----AGTCAAGCTTGAAGAAAAGCTTATTTTCCCAACCTCCCCAGAGTG 416
Db 644 CTGAAAACAAGCCATGACTTGAGAAAACAATTAATTTGATACCTGCTGCTTCTCAGAGT 703
QY 417 CAGTGTGACATTTTATTTAATTAACATCCACAAGA-GATTAATTTTAAATTAATTTAAAG 475
Db 704 GGTTCGAGATTTATTTAATCTAATTTCTAAGGAATAGAGCTTTATTAATTAATTAAT 763
QY 476 CATATATTTCTTAAAAAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 535
Db 764 CATGTTTCTTAAAGATTTTAA-----AAGTTAATTAATTTAATTAATTAATTAAT 814
QY 536 GTCATACATCTAGTGAATGTAAATGCAAAATCTGGTGATGTGTTTGTGTTTGTGTT 595
Db 815 TCCATGATTTTGTGGGTTTGAACATTAAGCCTTGATGATATATGATCATCTCAGTGCT 874

Oy 596 pp 597
Db 875 GT 876

RESULT 5
US-10-033-067-7

; Sequence 7, Application US/10033067
; Patent No. US20020164704A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROTEIN
; FILE REFERENCE: PF-0069-1 CON
; CURRENT APPLICATION NUMBER: US/10/033,067
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 08/683,655
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020164704A1 568961
; NAME/KEY: unsure
; LOCATION: 4, 12
; OTHER INFORMATION: a, t, c, g, or other
US-10-033-067-7

Query Match 28.5%; Score 244; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.6e-36;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 CCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCTCCAGATGAAGGTTCTGCAGCG 63
Db 13 CCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCTCCAGATGAAGGTTCTGCAGCG 72
Oy 64 CTTCTGTGCTGCTGCTCATGCGACGCCACTTTCAGCCCTCAGGACTTGTCTCAGCCAGAT 123
Db 73 CTTCTGTGCTGCTGCTCATGCGACGCCACTTTCAGCCCTCAGGACTTGTCTCAGCCAGAT 132
Oy 124 TCAGTTTCCATTCATCACTGCTGCTTTAAGTGATCAATAGGAAATTCCTATCCAG 183
Db 133 TCAGTTTCCATTCATCACTGCTGCTTTAAGTGATCAATAGGAAATTCCTATCCAG 192
Oy 184 AGGCTGGAGAGCTACACAGAATCACCAACATCCATGTCCCAAGGAAGCTGTGATCTTC 243
Db 193 AGGCTGGAGAGCTACACAGAATCACCAACATCCATGTCCCAAGGAAGCTGTGATCTTC 252

Oy 244 AAGA 247
Db 253 AAGA 256

RESULT 6
US-08-927-939-51
; Sequence 51, Application US/08927939
; Patent No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauren Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51

; LENGTH: 839
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)...(344)
US-08-927-939-51

Query Match 27.7%; Score 237; DB 8; Length 839;
Best Local Similarity 68.6%; Pred. No. 3.9e-35;
Matches 404; Conservative 0; Mismatches 170; Indels 15; Gaps 5;

Oy 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCTCCAGATGAAGGTTCTGCA 60
Db 9 AAACACACACCTCTCACGCCCAAGCTCACACCTTCAGCCTCCACATGAAGGTTCTCCGA 68
Oy 61 GCGCTTCTGTGCTGCTGCTCATGCGACGCCACTTTCAGCCCTCAGGACTTGTCTCAGCCA 120
Db 69 GCACTTCTGTGCTGCTGCTCATGCGACGCTGCTTCAAGCCCAAGGCTGCTGCGCCA 128
Oy 121 GATTCAGTTTCCATTCATCACTGCTGCTGCTTTAAGCTGATCAATAGGAAATTCCTATC 180
Db 129 GCTTCTG-----TCCCAACACACCTGCTGCTTTAACCCTGCGCAATAGGAAGATACCCCTT 182
Oy 181 CAGAGGCTGGAGAGCTACACAGAATCACCAACATCCATGTCGCCAAGGAAGCTGTGATC 240
Db 183 CAGGCACTAGAGAGCTACACAGAATCACCAAGTGGCAATGTCCCAAGAAAGCTGTGATC 242
Oy 241 TTCAGACCAAAACGGGCGCAGGAGGCTGTGCTGACCCCAAGAGAGAGATGGGTACAGGAT 300
Db 243 TTCAGACCAAACTGGCCAGGATATCTGTGCGCCAGCCCAAGAGAGAGATGGGTACAGGAT 302
Oy 301 TCCATGAAGCATCTGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATCATG-- 358
Db 303 TCCATGAAGTATCTGACCAAAATCTCCAACTCCAAAGCCATTAATATCACCATTCTT 362
Oy 359 GACTGAGAGTCAGAGCTTGAGAAAGCTTATTTATTTTCCCAACCTCCCCAGGTGCA 418
Db 363 GAAACCAAAACAGAGCTGAGTGTGCTTATTTGTTTC-----CCTTCTACAATGCA 417
Oy 419 GTGTGACATTTATTTATTTAATCAATCCACAAGA-GATTAATTTTAAATATTTAAAGCA 477
Db 418 TTCTGAGGTAACCTCATTTACGTCCAAAGGCGATGGGTTTATATATATATATATA 477
Oy 478 TAATATTTCTTAAAGATTTAATATATATTTAAGTGTGATGTTTAACTC-TATCTG 536
Db 478 TATTTTCTTAAAGATTTAATATATTTAAGTGTGATGTTTAACTC-TATCTCCT 537
Oy 537 TCATACATCTAGTGAATGTAAATGCCAAATCCTGCTGATGTCTTTT 585
Db 538 CCATGAATATCAGTTATTTTAAACTGTAAAGCTTGTGTCAGATTTCTT 586

RESULT 7
US-10-044-090-837
; Sequence 837, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 837
; LENGTH: 817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 222838.1
US-10-044-090-837

Query Match 27.5%; Score 235.6; DB 12; Length 817;
Best Local Similarity 67.7%; Pred. No. 6.9e-35;
Matches 409; Conservative 0; Mismatches 179; Indels 16; Gaps 5;

```
QY 1 AACCTTCACCTCTCATGCTGAAGCTCAGACCCCTTGCCCTCCAAGATGAAGTTCT-GC 59
    ||||| || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 26 AAACCTCCAATTCATGCTGAAGCCCAAGCCCTCACCCCTCCAACATGAAGCCTCTGGC 85
QY 60 AGCGCTCTGTGCT-GCTGCTCATGGAGCCACTTTTCAGCCCTCAGGAGCTTGCTCAGC 118
    ||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 86 AGCACTTCTGTGCTGTGCTGCTCAGAGAGCTGCTTTCAGCCCCCAGGGGCTTGCTCAGC 145
QY 119 CAGATTCAGTTTCCATTCACATCACCTGCTTTAACGTGATCAATAGAAATTCCTA 178
    ||| | || || || || || || || || || || || || || || || || || || || ||
Db 146 CAGTTGGGATTAATACTTCACTACCTGCTGTACAGATTATCAATAGAAATCCCTA 205
QY 179 TCCAGAGGCTGGAGAGCTACACAGAAATCAACATCCAATGTCCCAAGAAAGCTGTGA 238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 206 AGCAGAGGCTGGAGAGCTACAGAGAACCAACAGTAGCCACTGTCCCGGGAAGCTGTAA 265
QY 239 TCTTCAGAGCAAAACGGGCAAGGAGTGTGCTGACCCCAAGAGAGATGGGTCAAGG 298
    ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 266 TCTTCAGAGCAAAACCTGAGCAAGAGATCTGTGACCCACACAGAGTGGGTCCAGG 325
QY 299 ATTCCATGAAGCATCTGACCAAAATATTCAAAATCTGAAGCCATGAGCCTTCATACATG 358
    | | ||||| ||||| || || || || || || || || || || || || || || ||
Db 326 ACTTATGAAGCACTGACAGAAACCAACCTCCAAGCTTGAACATTCATGACTG 385
QY 359 GACTGAG----AGTCAGAGCTGAAGAAAGCTTATTATTTCGCCCAACCTCCCCAGG 414
    ||||| || || || ||||| || || || || || || || || || || || || || ||
Db 386 AACTGAACAAGCCATGACTGAGAAACAATTAATTGTATACCTGTCTTCTCAGA 445
QY 415 TGCAGTGTGACATTTATTATTATTAACATCCACAAGA-GATTATTTTAAATAATTAA 473
    || || || || ||||| || || || || || || || || || || || || || || ||
Db 446 GTGTTCTGAGATTATTTAATCTAATCTAAGGAATATGAGCTTATGTAATATGTA 505
QY 474 AGCATATATTTCTTAAAAAGATTTAATATTAATTAAAGTTGATGTTTAACTCTAT 533
    | ||| | ||||| | | | | | ||||| | | | | | ||||| | | |
Db 506 ATCATGTTTCTTAGATATTTAA-----AAGTTATTAATATTTAATTTAAT 556
QY 534 CTGTCAATACATCCTAGTAGATGTAATAATGCAAAATCCTGATGTGTTTGTGTTTG 593
    || || || || || || || || || || || || || || || || || || || || ||
Db 557 CTTCATGATTTTGTGGGTTTGAACATAAAGCCTTGATGTATATGTCATCTCAGTG 616
QY 594 TTTT 597
    | |
Db 617 CTGT 620
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RESULT 8
US-10-044-090-494
; Sequence 494, Application us/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 494
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 222839.1
US-10-044-090-494

Query Match 27.0%; Score 230.8; DB 12; Length 987;
Best Local Similarity 68.0%; Pred. No. 5.5e-34;

Matches 400; Conservative 0; Mismatches 172; Indels 16; Gaps 5;

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QY 1 AACCTTCACCTCTCATGCTGAAGCTCAGACCCCTTGCCCTCCAAGATGAAGTTCTGCA 60
    ||||| ||||| || ||||| || ||||| || ||||| ||||| ||||| ||||| |||||
Db 159 AAACCAACCACTCTCAGCCCAAAAGCTCACACCTTCAGCCTCCAACATGAAGTCTCCGA 218
QY 61 GCGCTTCTGTGCTGCTGCTCATGGAGCCACTTTTCAGCCCTCAGGAGCTTGCTCAGCCA 120
    || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| || || || || ||
Db 219 GCACTTCTGTGCTGCTGCTCATAGCAGCTGCTTCAGCCCCCAGGGGCTCACTGGGCA 278
QY 121 GATTCAGTTTCCATTCCAATCACCTGCTGCTTTAACGTGATCAATAGAAATTCCTATC 180
    | ||| | || || ||||| ||||| ||||| ||||| || ||||| || || || || ||
Db 279 GCTCTG-----TCCCAACCACTGCTGCTTTAACCTGGCCAATAGGAAGATACCCCTT 332
QY 181 CAGAGGCTGGAGAGCTACACAAGAATCACCAACATCCATGTCCCAAGAGAGCTGTGATC 240
    || | | ||||| || ||||| ||||| ||||| ||||| || ||||| || ||||| || ||
Db 333 CAGGACTAGAGAGCTACAGGAATCACCAAGTGGCAATGTCCCAAGAAAGCTGTGATC 392
QY 241 TTCAGAGCAAAACGGGCAAGAGGCTGCTGCTGACCCCAAGAGAGATGGGTCAAGGAT 300
    ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||
Db 393 TTCAAGACCAACTGGCCAAGATATCTGTGCCGACCCCAAGAAGAAGTGGGTGAGAT 452
QY 301 TCCATGAAGCATCTGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATG-- 358
    ||||| ||||| ||||| || || || || || || || || || || || || || || ||
Db 453 TCCATGAAGTATCTGACCAAAATCTCCAACCTCCAAGCCATAATATACCATTTT 512
QY 359 GACTGAGAGTCAGAGCTGAAGAAAGCTTATTATTTCGCCCAACCTCCCCAGGTGCA 418
    || | | ||||| || || || || || || || || || || || || || || || ||
Db 513 GAAACCAAAACAGAGCTGAGTGTGCTTAATTGTTC-----CCTCTTACAATGCA 567
QY 419 GTGTGACATTATTTATTAATCAATCCACAAGAGATATTTTAAATAATTTAAAGCAT 478
    || || | | ||||| || | || || || || || || || || || || || || || ||
Db 568 TTCTGAGTAACCTCATTA--CAGTCCAAGGGCATGGCTTTATATATATATATATA 625
QY 479 AATATTTCTTAAAGATTTAATATATATTAAGTTGTGATGTTTAACCTC-TATCTGT 537
    | ||| ||||| | || ||||| || ||||| || ||||| || || || || || || ||
Db 626 TTTTAAAAAAGATATTTGATTTAATTTAATTTAAGGCTTTAAACTTATCTTC 685
QY 538 CATACATCCTAGTGAATGAATAATGCAAAATCCTGCTGATGTGTTT 585
    || | | || || || || || || || || || || || || || || || || || ||
Db 686 CATGAATATCAGTTATTTTAAACTGTAAAGCTTTGTGAGATTTCTT 733
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RESULT 9
US-08-927-939-76
; Sequence 76, Application US/08927939
; Patent No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Granger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(331)
US-08-927-939-76

Query Match 26.6%; Score 227.8; DB 8; Length 685;
Best Local Similarity 63.8%; Pred. No. 1.8e-33;
Matches 370; Conservative 9; Mismatches 198; Indels 3; Gaps 3;

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Db 1 TCAAACTGAAGCTCGCACTCTCGCC-TCCAGCATGAAGATCTGCGCCCTTCTGTGCC 59
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QY 194 GCTACACAGAATCACCAACATCCATGTCGCCAAGGAAGCTGTGATCTTCAAGACCAAAC 253
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QY 254 GGGCAAGAGGCTGCTGCTGAGCCCAAGAGAGATGGGTGAGGATTCATGAGCATC 313
Db 240 TGGCCAAGGAGATGCTGCTGAGCCCAAGCAGAGTGGGTTCAGGATTCATGAGCATC 299
QY 314 TGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGAGCTGAGAGTCAGAG 373
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QY 494 GTATTTAATTAATTAAGTGTGATGTTTAACTCTATCTGTCATACATCCAGTGA 553
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Db 538 TTTTAGATACAGAGACTTGGGGAATTGCTTTTCCPTTG 577

RESULT 10

US-09-981-876-106
; Sequence 106, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
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; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 106
; LENGTH: 1712
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Query Match          26.0%; Score 222.6; DB 9; Length 1712;
Best Local Similarity 68.3%; Pred. No. 2e-32;
Matches 405; Conservative 1; Mismatches 160; Indels 27; Gaps 6;
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QY 181 CAGAGGCTGAGAGCTTACAGAAATCACCAACATCCATGTCCCAAGGAAGCTGTGATC 240
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US-09-148-545-106
; Sequence 106, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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: EARLIER APPLICATION NUMBER: 60/047,590
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: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/057,650
: EARLIER FILING DATE: 1997-09-05
: EARLIER APPLICATION NUMBER: 60/056,884
: EARLIER FILING DATE: 1997-08-22
: NUMBER OF SEQ ID NOS: 280
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 106
: LENGTH: 1712

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; Sequence 105, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
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; PRIOR FILING DATE: 1997-05-23

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; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 1822

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Query Match	26.08;	Score 222.6;	DB 9;	Length 1822;
Best Local Similarity	68.38;	Pred. No. 2e-32;		
Matches 405; Conservative	1;	Mismatches 160;	Indels 27;	Gaps 62;

OY	1	AAACCTTCACCCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAAGATGAAGTTTCTGCA	60
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Dd	1466	GTGACATTTATTTATTAACATCCACAAAGAGATTATTTTAAATAATTTAAGCATAA	1509
OY	481	TATTTCTTAAAAAGTATTTAATTTATTTAAGTGTGATGTTTTTAACTCTATCTGCAT	540
Dd	1510	TATGCTTAAAGTATTTAATTTCTTATTTAAGTATTTGATGTTTTTAAAGTTATCTTTCAT	1569
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RESULT 13

US-09-148-545-105
: Sequence 105, Application US/09148545
: Publication No. US20030027132A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: 70 Human Secreted Proteins
: FILE REFERENCE: P2001P1
: CURRENT APPLICATION NUMBER: US/09/148, 545
: CURRENT FILING DATE: 1998-09-04
: EARLIER APPLICATION NUMBER: PCT/US98/04482
: EARLIER FILING DATE: 1998-03-06
: EARLIER APPLICATION NUMBER: 60/040,162
: EARLIER FILING DATE: 1997-03-07
: EARLIER APPLICATION NUMBER: 60/040,333
: EARLIER FILING DATE: 1997-03-07
: EARLIER APPLICATION NUMBER: 60/038,621
: EARLIER FILING DATE: 1997-03-07
: EARLIER APPLICATION NUMBER: 60/040,161
: EARLIER FILING DATE: 1997-03-07
: EARLIER APPLICATION NUMBER: 60/040,626

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EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/043,578

EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,908
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EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 105
LENGTH: 1822

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Best Local Similarity 68.3%; Pred. No. 2e-32;
Matches 405; Conservative 1; Mismatches 160; Indels 27; Gaps 6;

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Db 1115 GCCCTTCTGTGCTGCTGCTGCTATAGCAGCCACCTTCATTCGCCAAGGCTCGCTCAGCCA 1174
QY 121 GATTCAAGTTTCCATTCCAAATCACTGCTGCTTTAAGTGATCAATAGAAATTCCTATC 180
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QY 181 CAGAGGCTGGAGAGCTACACAGAAATCACCAACATCCAAATGTCACCAAGGAAGCTGTGATC 240
Db 1235 CAGAGGCTCGGAGCTATAGAGAAATCACCAAGCAAGAGTGTCACCAAGGAAGCTGTGATC 1294
QY 241 TTCAAGACCAAAACGGGGCAGGAGGCTGTGCTGACCCCAAGGAGATGGGTGAGGAT 300
Db 1295 TTCAAGACCAATGTGGCCAGGAGATCTGTGCTGACCCCAAGGAGATGGGTGAGGAT 1354
QY 301 TCCATGAAGCATCTGAGCAAAATATTTCAAAATCTGAAGCAATGAGCCTTCATACATGGA 360
Db 1355 TCCATGAGCACCTGAGCAAGCAAAACCAACTCGAAGACTGACACTCCACAA 1414
QY 361 CTGAGAGTCAGAGCTGAAGAAAGCTTATTTATTTCCCAACTCCCCAGTGAGT 420
Db 1415 CCCA-----AGATCTGACGTAA-----CTATTTTCCCTGAGCTTCCCCAGACACCCCT 1465
QY 421 GTGACATTTATTTATATATCATCCACAAGAGATTTATTTAAATTAATTTAAAGCATAA 480
Db 1466 GTTTTATTTATATAT-----GAATTTTGTGTGATGTGAACAT-- 1509
QY 481 TATTTCTTAAAAAGTATTTAATATATTTAAGTGTGATGTTTAACTCTATCTGTGAT 540

Db 1510 TATGCCTTAAGTAATGTTAATTTCTATTAGTTATGTGATGTTTTTAAGTTTACTTTTCAT 1569
QY 541 ACATCCTAGTGAATGTAATAATGCAAAAATCCTGTGATGTGTTTTTTTGTGTTTG 593
Db 1570 GG-TACTAGTGTGTTTTTTAGATACAGAGACTGTGGGAAATGCTTTTCCCTCTG 1621

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US-10-044-090-583

; Sequence 583, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 583
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 452327CB1
US-10-044-090-583

Query Match 25.9%; Score 221.4; DB 12; Length 804;
Best Local Similarity 68.3%; Pred. No. 2.8e-32;
Matches 405; Conservative 0; Mismatches 161; Indels 27; Gaps 6;

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Db 74 AAACATCCAAATTTCTCAAACTGAAGCTCGACTCTCG-CCTCCAGCATGAAGTCTCTGCC 132
QY 61 GCGCTTCTGTGCTGCTGCTCATGCGAGCCACTTTCAAGCCCTCAGGGAGCTTGTGAGCCA 120
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QY 121 GATTCAGTTTCCATTTCCAAATCACCTGCTGCTTTAAAGTGATCAATAGAAATTCCTATC 180
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US-10-044-090-822
; Sequence 822, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 822
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 223187CB1
US-10-044-090-822

Query Match 25.6%; Score 218.8; DB 12; Length 600;
Best Local Similarity 75.1%; Pred. No. 7.9e-32;
Matches 302; Conservative 0; Mismatches 92; Indels 8; Gaps 2;

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QY 121 GATTCAGTTTCCATTTCCAAATCACCTGCTGCTTTAAAGTGATCAATAGAAATTCCTATC 180
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Job time : 84 secs

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OM nucleic - nucleic search, using sw model

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Title: US-10-033-067-2
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 848478

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Maximum Match 100%
Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	849	99.2	856	9 US-10-033-067-2	Sequence 2, Appli
2	842.2	98.4	870	12 US-10-044-090-581	Sequence 581, App
3	841	98.2	2738	8 US-08-927-939-80	Sequence 80, Appl
4	257.6	30.1	1085	8 US-08-927-939-81	Sequence 81, Appl
5	244	28.5	256	9 US-10-033-067-7	Sequence 7, Appli
6	237	27.7	839	8 US-08-927-939-51	Sequence 51, Appl
7	235.6	27.5	817	12 US-10-044-090-837	Sequence 837, App
8	230.8	27.0	987	12 US-10-044-090-494	Sequence 494, App
9	227.8	26.6	685	8 US-08-927-939-76	Sequence 76, Appl
10	222.6	26.0	1712	9 US-09-981-876-106	Sequence 106, App
11	222.6	26.0	1712	9 US-09-148-545-106	Sequence 106, App
12	222.6	26.0	1822	9 US-09-981-876-105	Sequence 105, App
13	222.6	26.0	1822	9 US-09-148-545-105	Sequence 105, App
14	221.4	25.9	804	12 US-10-044-090-583	Sequence 583, App
15	218.8	25.6	600	12 US-10-044-090-822	Sequence 822, App
16	216.4	25.3	383	9 US-10-114-893-51	Sequence 51, Appl
17	213	24.9	236	9 US-10-033-067-5	Sequence 5, Appli
18	204	23.8	647	10 US-09-777-430A-72	Sequence 72, Appl
19	203	23.7	825	8 US-08-927-939-28	Sequence 28, Appl

20	203	23.7	825	8 US-08-927-939-33	Sequence 33, Appl
21	203	23.7	832	12 US-10-044-090-838	Sequence 838, App
22	203	23.7	860	10 US-09-872-611A-3	Sequence 3, Appli
23	199.4	23.3	228	9 US-10-033-067-6	Sequence 6, Appli
24	194	22.7	338	9 US-10-040-739-793	Sequence 793, App
25	183.4	21.4	289	9 US-10-057-275-1	Sequence 1, Appli
26	170.4	19.9	297	9 US-10-164-621-3	Sequence 3, Appli
27	170.4	19.9	297	9 US-10-125-451-3	Sequence 3, Appli
28	168.8	19.7	297	10 US-09-872-611A-1	Sequence 1, Appli
29	154.8	18.1	258	9 US-09-796-692-7869	Sequence 7869, Ap
30	149.2	17.4	972	9 US-09-792-793A-61	Sequence 61, Appl
31	149.2	17.4	978	9 US-09-792-793A-62	Sequence 62, Appl
32	149.2	17.4	993	9 US-09-792-793A-63	Sequence 63, Appl
33	139	16.2	978	9 US-09-792-793A-52	Sequence 52, Appl
34	139	16.2	984	9 US-09-792-793A-53	Sequence 53, Appl
35	139	16.2	999	9 US-09-792-793A-54	Sequence 54, Appl
36	119.2	13.9	253	10 US-09-833-381-1229	Sequence 1229, Ap
37	110.4	12.9	453	10 US-09-864-761-1789	Sequence 1789, Ap
38	104.4	12.2	476	10 US-09-864-761-5570	Sequence 5570, Ap
39	102.2	11.9	400	10 US-09-833-381-1234	Sequence 1234, Ap
40	99.8	11.7	724	12 US-10-044-090-839	Sequence 839, App
41	93.8	11.0	231	9 US-09-792-793A-67	Sequence 67, Appl
42	93.8	11.0	978	9 US-09-792-793A-55	Sequence 55, Appl
43	93.8	11.0	984	9 US-09-792-793A-56	Sequence 56, Appl
44	93.8	11.0	999	9 US-09-792-793A-57	Sequence 57, Appl
45	79.6	9.3	360	10 US-09-864-761-5454	Sequence 5454, Ap

ALIGNMENTS

RESULT 1
US-10-033-067-2
; Sequence 2, Application US/10033067
; Patent No. US20020164704A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROTEIN
; FILE REFERENCE: PE-0069-1 CON
; CURRENT APPLICATION NUMBER: US/10/033,067
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 08/683,655
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020164704A1. 965517CB1
; NAME/KEY: unsure
; LOCATION: 628, 650, 653, 676, 769, 779, 820
; OTHER INFORMATION: a, t, c, g, or other
US-10-033-067-2

Query Match 99.2%: Score 849; DB 9; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.9e-147;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	AAACCTTCACTCTCATGCTGAAGCTCACACCCCTGCCCTCCAAGATGAAGTTCTGCA	60
QY	61	GCGCTTCTGTGCTGCTGCTCATGGAGCCACTTTCAGCCCTCAGGACTTGTCTAGCCA	120
Db	61	GCGCTTCTGTGCTGCTGCTCATGGAGCCACTTTCAGCCCTCAGGACTTGTCTAGCCA	120
QY	121	GATTCAGTTTCCATTCACATCACCTGCTGCTTAACGTGATCAATGAATAATTCCTATC	180

Db 121 GATTCAGTTTCCATTCCAATCACCCTGCTGCTTTTAACGTGATCAATAGAAAAATTCCTATC 180
OY 181 CAGAGCTGAGAGCTACACAGAATCACCAACATCCATATGTCCTCAAGAGAGCTGTGATC 240
Db 181 CAGAGCTGAGAGCTACACAGAATCACCAACATCCATATGTCCTCAAGAGAGCTGTGATC 240
OY 241 TTCAAGACCAACGGGGCAAGAGAGCTGTGCTGACCCCAAGAGAGAGATGGGTCAAGGAT 300
Db 241 TTCAAGACCAACGGGGCAAGAGAGCTGTGCTGACCCCAAGAGAGAGATGGGTCAAGGAT 300
OY 301 TCCATGAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 360
Db 301 TCCATGAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 360
OY 361 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTTATTTCCCAACCTCCCAAGGTGCAGT 420
Db 361 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTTATTTCCCAACCTCCCAAGGTGCAGT 420
OY 421 GTGACATTTATTTATTAACATCCACAAAGAGATTTTAAATAATTAAAGCATAA 480
Db 421 GTGACATTTATTTATTAACATCCACAAAGAGATTTTAAATAATTAAAGCATAA 480
OY 481 TATTTCTTAAAAAGTATTTAATTTAAGTTGTGATGTTTAACTCTATCTGTCAT 540
Db 481 TATTTCTTAAAAAGTATTTAATTTAAGTTGTGATGTTTAACTCTATCTGTCAT 540
OY 541 ACATCCTAGTGAATGTAAATGCAAAATCCTGTGATGTTTGTGTTTGTTCCT 600
Db 541 ACATCCTAGTGAATGTAAATGCAAAATCCTGTGATGTTTGTGTTTGTTCCT 600
OY 601 GTGAGCTCAACTAAGTTCACGGCCAAANGTCAATGTTCTCCCTACCCNGTNGTAGTG 660
Db 601 GTGAGCTCAACTAAGTTCACGGCCAAANGTCAATGTTCTCCCTACCCNGTNGTAGTG 660
OY 661 TTGTGGGCTCCTCCNTGGATCATCAAGGTGAACACTTAGGTATCTTGGCAATCAGT 720
Db 661 TTGTGGGCTCCTCCNTGGATCATCAAGGTGAACACTTAGGTATCTTGGCAATCAGT 720
OY 721 GCTCCTGTAAGTCAAAATGTGTGCTTGTACTGCTGTGTAATTGANGTTACTGTANA 780
Db 721 GCTCCTGTAAGTCAAAATGTGTGCTTGTACTGCTGTGTAATTGANGTTACTGTANA 780
OY 781 TAACATATGGAATTTGAAAAAATTTCAAAAAAANATATATATTAATTTAAACTA 840
Db 781 TAACATATGGAATTTGAAAAAATTTCAAAAAAANATATATATTAATTTAAACTA 840
OY 841 AAAAAAAAAAAAAAAAAA 856
Db 841 AAAAAAAAAAAAAAAAAA 856

RESULT 2
US-10-044-090-581
; Sequence 581, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 581
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 2883526CB1
US-10-044-090-581

Query Match 98.4%; Score 842.2; DB 12; Length 870;

Best Local Similarity 98.8%; Pred. No. 3.3e-146;
Matches 844; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAGATGAAGTTCTGCA 60
Db 17 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAGATGAAGTTCTGCA 76
OY 61 GCGCTTCTGTGCTGCTGCTCATGCGCAGCCACTTTCAGCCCTTCAGGGACTTGCTCAGCCA 120
Db 77 GCGCTTCTGTGCTGCTGCTCATGCGCAGCCACTTTCAGCCCTTCAGGGACTTGCTCAGCCA 136
OY 121 GATTCAGTTTCCATTCACATCACCCTGCTGCTTTAACGTGATCAATAGGAAATTCCTATC 180
Db 137 GATTCAGTTTCCATTCACATCACCCTGCTGCTTTAACGTGATCAATAGGAAATTCCTATC 196
OY 181 CAGAGCTGAGAGCTACACAGAATCACCAACATCCAAATGTGCCAAGGAAGCTGTGATC 240
Db 197 CAGAGCTGAGAGCTACACAGAATCACCAACATCCAAATGTGCCAAGGAAGCTGTGATC 256
OY 241 TTCAAGACCAACGGGGCAAGAGAGTCTGTGCTGACCCCAAGAGAGAGATGGGTCAAGGAT 300
Db 257 TTCAAGACCAACGGGGCAAGAGAGTCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT 316
OY 301 TCCATGAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 360
Db 317 TCCATGAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 376
OY 361 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTTTCCCAACCTCCCAAGGTGCAGT 420
Db 377 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTTATTTCCCAACCTCCCAAGGTGCAGT 436
OY 421 GTGACATTTATTTATTAACATCCACAAAGAGATTTTAAATAATTAAAGCATAA 480
Db 437 GTGACATTTATTTATTAACATCCACAAAGAGATTTTAAATAATTAAAGCATAA 496
OY 481 TATTTCTTAAAAAGTATTTAATTAATTTAAGTTGTGATGTTTAACTCTATCTGTCAT 540
Db 497 TATTTCTTAAAAAGTATTTAATTAATTTAAGTTGTGATGTTTAACTCTATCTGTCAT 556
OY 541 ACATCCTAGTGAATGTAAATGCAAAATCCTGTGATGTTTGTGTTTGTTCCT 600
Db 557 ACATCCTAGTGAATGTAAATGCAAAATCCTGTGATGTTTGTGTTTGTTCCT 616
OY 601 GTGAGCTCAACTAAGTTCACGGCCAAANGTCAATGTTCTCCCTCCACNGTNGTAGTG 660
Db 617 GTGAGCTCAACTAAGTTCACGGCCAAANGTCAATGTTCTCCCTCCACNGTNGTAGTG 676
OY 661 TTGTGGGCTCCTCCNTGGATCATCAAGGTGAACACTTAGGTATCTTGGCAATCAGT 720
Db 677 TTGTGGGCTCCTCCATGGATCATCAAGGTGAACACTTAGGTATCTTGGCAATCAGT 736
OY 721 GCTCCTGTAAGTCAAAATGTGTGCTTGTACTGCTGTTGTAATTTGANGTTACTGTANA 780
Db 737 GCTCCTGTAAGTCAAAATGTGTGCTTGTACTGCTGTTGTAATTTGANGTTACTGTATA 796
OY 781 TAACATATGGAATTTGAAAAAATTTCAAAAAAANATATATATTAATTTAAACTA 840
Db 797 TAACATATGGAATTTGAAAAAATTTCAAAAAAANATATATATTAATTTAAACTA 856
OY 841 AAAAAAAAAAAAAAAAAA 854
Db 857 AAAAAAAAAAAAAAAAAA 870

RESULT 3
US-08-927-939-80
; Sequence 80, Application US/08927939
; Patent No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.

FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 2738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (123)...(353)
US-08-927-939-80

Query Match 98.2%; Score 841; DB 8; Length 2738;
Best Local Similarity 98.6%; Pred. No. 7e-146;
Matches 844; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCTCCAGATGAAGGTTCTGCA 60
Db 12 AACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCTCCAGATGAAGGTTCTGCA 71
QY 61 GCGCTTCTGTGCTGCTGCTCATGCGAGCCACTTTCAGCCCTCAGGGACTGCTCAGCCA 120
Db 72 GCGCTTCTGTGCTGCTGCTCATGCGAGCCACTTTCAGCCCTCAGGGACTGCTCAGCCA 131
QY 121 GATTCAGTTTCCATTCCAATCACCTGCTGCTTAACTGATCAATAGGAAATTCCTATC 180
Db 132 GATTCAGTTTCCATTCCAATCACCTGCTGCTTAACTGATCAATAGGAAATTCCTATC 191
QY 181 CAGAGGCTGAGAGCTACACAAGAATCACCAACATCCAAATGCCAAGGAAGCTGTGATC 240
Db 192 CAGAGGCTGAGAGCTACACAAGAATCACCAACATCCAAATGCCAAGGAAGCTGTGATC 251
QY 241 TTCAGAGCCAAACGGGGCAAGAGGCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT 300
Db 252 TTCAGAGCCCAACGGGGCAAGAGGCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT 311
QY 301 TCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGA 360
Db 312 TCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGA 371
QY 361 CTGAGAGTCAGAGCTTGAGAAAGCCTTATTTTCCCAACCTCCCCAGAGTGCAGT 420
Db 372 CTGAGAGTCAGAGCTTGAGAAAGCCTTATTTTCCCAACCTCCCCAGAGTGCAGT 431
QY 421 GTGACATTATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
Db 432 GTGACATTATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 491
QY 481 TATTTCTTAAAAAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
Db 492 TATTTCTTAAAAAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 551
QY 541 ACATCCTAGTGAATGTAATAATGCAAAATCCTGGTGAATGTTTTTTGTTTCTTCT 600
Db 552 ACATCCTAGTGAATGTAATAATGCAAAATCCTGGTGAATGTTTTTTGTTTCTTCT 611
QY 601 GTGAGCTCAACTAAGTCAAGGCCCAANGTCATGTTCTCCCTCCTACCTGCTAGT 660
Db 612 GTGAGCTCAACTAAGTCAAGGCCCAANGTCATGTTCTCCCTCCTACCTGCTAGT 671
QY 661 TTGTGGGCTCCTCCNTGATCATCAAGGTGAACACCTTAGTATTTCTTTGCAATCAGT 720
Db 672 TTGTGGGCTCCTCCATGATCATCAAGGTGAACACCTTAGTATTTCTTTGCAATCAGT 731
QY 721 GCTCCTGTAGTCAAAATGTGCTTTGTACTGCTGTGTGAATTTGANGTACTGTANA 780
Db 732 GCTCCTGTAGTCAAAATGTGCTTTGTACTGCTGTGTGAATTTGANGTACTGTANA 791
QY 781 TAACATATGAATTTGAAAAAAATTTCAAAAAAGAAAAANATATATTAATTTAAACTA 840
Db 792 TAACATATGAATTTGAAAAAAATTTCAAAAAAGAAAAANATATATTAATTTAAACTA 851

QY 841 AAAAAAAAAAAAAA 856
Db 852 AGAAAAAAAAAAAAA 867

RESULT 4

US-08-927-939-81
; Sequence 81, Application US/08927939
; Patent No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Gralinger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 1085
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (329)...(625)
US-08-927-939-81

Query Match 30.1%; Score 257.6; DB 8; Length 1085;
Best Local Similarity 67.9%; Pred. No. 6.8e-39;
Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;

QY 1 AACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCTCCAGATGAAGGTTCTGCA 60
Db 284 AACCTTCACCTCTCATGCTGAAGGCCCATGCCCTCACCTCCAAATGAAGCCTCTGCA 343
QY 61 GCGCTTCTGTGCTGCTGCTCATGCGAGCCACTTTCAGCCCTCAGGGACTGCTCAGCCA 120
Db 344 GCACCTTCTGTGCTGCTGCTCATGCGAGCAGCTGCTTTCAGCCCCAGGGCTTGTCTCAGCCA 403
QY 121 GATTCAGTTTCCATTCCAATCACCTGCTGCTTAACTGATCAATAGGAAATTCCTATC 180
Db 404 GTTGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 463
QY 181 CAGAGGCTGAGAGCTACACAAGAATCACCAACATCCAAATGTCCCAAGGAAGCTGTGATC 240
Db 464 CAGAGGCTGAGAGCTACACAAGAAGCACCAAGTAGCCACTGTCCCCGGGAAGCTGTAATC 523
QY 241 TTCAGAGCCAAACGGGGCAAGAGGCTGTGCTGACCCCAAGGAGAGATGGTCAAGGAT 300
Db 524 TTCAGAGCCAAACGGGGCAAGAGGATGTGCTGACCCCAAGGAGAGTGGTCCAGGAC 583
QY 301 TCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGA 360
Db 584 TTTATGAAGCACTGGACAAAGAAACCAACTCCAAAGCTTTGAACATTCATGACTGAA 643
QY 361 CTGAG---AGTCAGAGCTTGAAGAAAGCTTATTTATTTTCCCAACCTGCCAGGTG 416
Db 644 CTGAAACCAAGCCATGACTTGAGAAACAATAATTTGTATACCTGTCTTCTCAGAGT 703
QY 417 CAGTGTGACATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 475
Db 704 GGTTCGAGATTAATTTTAATCTAATTTGAAGGAATATGAGCTTATATGAATGTAAT 763
QY 476 CATATATTTCTTAAAAAGTATTTAATTAATTAATTTAAGTTGTGANGTTTAACTCTATCT 535
Db 764 CATGTTTCTTCTAGTATTTTAA-----AAGTATTAATTAATTTAATCT 814
QY 536 GTCATACATCCTAGTGAATGTAATAATGCAAAATCCTGGTGAATGTTTGTGTTTGTGT 595
Db 815 TCCATGATTTTGGTGGTTTGAACATTAAGCCTTGATGATATATGTCATCTCAGTGTCT 874

OY 596 TTT 597
1
Db 875 GT 876

RESULT 5

US-10-033-067-7
; Sequence 7, Application US/10033067
; Patent No. US20020164704A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROTEIN
; FILE REFERENCE: PF-0069-1 CON
; CURRENT APPLICATION NUMBER: US/10/033,067
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 08/683,655
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020164704A1 568961
; NAME/KEY: unsure
; LOCATION: 4, 12
; OTHER INFORMATION: a, t, c, g, or other
US-10-033-067-7

Query Match 28.5%; Score 244; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.6e-36;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCTTCACCTCTCATGCTGAAGCTCACACCTTGCCCTCAAGATGAAGTTTCTGCAGCG 63
Db 13 CCTTCACCTCTCATGCTGAAGCTCACACCTTGCCCTCAAGATGAAGTTTCTGCAGCG 72
OY 64 CTTCGTGCTGCTGCTCATGCGCAGCCACTTTACGCCCTCAGGACTTGTCCAGCCAGAT 123
Db 73 CTTCGTGCTGCTGCTCATGCGCAGCCACTTTACGCCCTCAGGACTTGTCCAGCCAGAT 132
OY 124 TCAGTTCCATTCACATCACCTGCTGCTTTAAGTGATCATAGGAAATTCCTATCCAG 183
Db 133 TCAGTTCCATTCACATCACCTGCTGCTTTAAGTGATCATAGGAAATTCCTATCCAG 192
OY 184 AGCGTGAGAGCTACACAGAATCACCAACATCCCAATGTCCCAAGAGCTGTGATCTTC 243
Db 193 AGCGTGAGAGCTACACAGAATCACCAACATCCCAATGTCCCAAGAGCTGTGATCTTC 252

OY 244 AAGA 247
1111
Db 253 AAGA 256

RESULT 6

US-08-927-939-51
; Sequence 51, Application US/08927939
; Patent No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51

; LENGTH: 839
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)...(344)
US-08-927-939-51

Query Match 27.7%; Score 237; DB 8; Length 839;
Best Local Similarity 68.6%; Pred. No. 3.9e-35;
Matches 404; Conservative 0; Mismatches 170; Indels 15; Gaps 5;

OY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCTTGCCCTCAAGATGAAGTTTCTGCA 60
Db 9 AAACACACACCTCTCATGCTGAAGCTCACACCTTGCCCTCAAGATGAAGTTTCTGCA 68
OY 61 GCGCTTCTGTGCTGCTGCTCATGCGCAGCCACTTTACGCCCTCAGGACTTGTCCAGCCA 120
Db 69 GCACTTCTGTGCTGCTGCTCATGAGAGCTGCTGAGCCCAAGGGCTGCTGAGCCA 128
OY 121 GATTCAGTTTCCATTCACATCACCTGCTGCTTTAAGTGATCATAGGAAATTCCTATC 180
Db 129 GCTTCTG-----TCCCAACCACTGCTGCTTTAACCCTGGCCAATAGGAGATACCCCTT 182
OY 181 CAGAGGCTGAGAGCTACACAGAATCACCAACATCCATGTCCCAAGAGCTGTGATC 240
Db 183 CAGGACTAGAGAGCTACAGAGATCACCAAGTGGAATGTCCCAAGAGCTGTGATC 242
OY 241 TTCAAGACCAACCGGCAAGAGAGTCTGTGCTGAGCCCAAGAGAGATGGTCAAGGAT 300
Db 243 TTCAAGACCAAACTGGCCAAAGATATCTGTGCGCAGCCCAAGAGAGATGGTCAAGAT 302
OY 301 TCCATGAAGCATCTGACCAAAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATG-- 358
Db 303 TCCATGAAGTATCTGACCAAAATCTCCAACTCCAAAGCCATAAATATCACCATTTT 362
OY 359 GACTGAGAGTCAGAGCTTGAAGAAAGCTTATTTTCCCAACCTCCCCAGGTGCA 418
Db 363 GAAACCAACAGAGAGCTGAGTGTGCTTATTTTTC-----CCTCTTACAATGCA 417
OY 419 GTGTGACATTTATTTATTAACATCCACAAGA-GATTATTTTAAATATTAAGCA 477
Db 418 TTCTGAGTAACTTCATATTCAGTCCAAAGGCGATGGTTTATATATATATATATA 477
OY 478 TAATATTTCTTAAAAAGTATTTAATTAATTAAGTGTGATGTTTAACTC-TATCTG 536
Db 478 TATTTTAAAAAAGTATTTAATTAATTAAGTGTGATGTTTAAACTTATCTT 537
OY 537 TCATACATCTAGTGAATGTAATAATGCAAAATCCTGCTGATGTTTTT 585
Db 538 CCATGAATATCAGTTATTTTAAACTGTAAAGCTTTGTGAGATTTCTT 586

RESULT 7

US-10-044-090-837
; Sequence 837, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 837
; LENGTH: 817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 222838.1
US-10-044-090-837

Query Match 27.58; Score 235.6; DB 12; Length 817;
Best Local Similarity 67.78; Pred. No. 6.9e-35;
Matches 409; Conservative 0; Mismatches 179; Indels 16; Gaps 5;

QY 1 AACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAAGATGAAGTTTCT-GC 59
Db 26 AAACCTCCAATTCATGTGGAAGCCCATGCCCCTCACCTCCAACATGAAGCCTGTGCG 85
QY 60 AGCGCTTCTGTGCTT-GCTGCTCATGCGAGCCACCTTTCAGCCCTCAGGAGCTGTGCTCAGC 118
Db 86 AGCACTTCTGTGCTGTGCTGCTCACAGCAGCTGTTCAGCCCCCAGGGGCTGTGCTCAGC 145
QY 119 CAGATTCAAGTTTCCATTCACATCACCTGCTGCTTAAAGTGAATAGAAATTCCTA 178
Db 146 CAGTTGGATTATTAATCTCACTACCTGCTGCTACAGATTATCAATAAGAAATCCCTA 205
QY 179 TCCAGAGGCTGGAGAGCTACACAGAATCACCAACATCCATGTCCCAAGGAAGCTGTGA 238
Db 206 AGCAGAGGCTGGAGAGCTACAGAAAGGACCACAGTAGCCACTGTCCCCGGGAAGCTGTAA 265
QY 239 TCTTCAGACCAAAACGGGCAAGGAGGTCTGTGCTGACCCCAAGGAGAGATGGGTCAAGG 298
Db 266 TCTTCAAGACCAAACTGACAGAAGAGATCTGTGCTGACCCACACAGAAGTGGGTCCAGG 325
QY 299 ATTCCATGAAGCATCTGACCAATAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATG 358
Db 326 ACTTTATGAAGCACCCTGACAGAAGAAACCCAACTCCAAGCTTTGAACATTCATGACTG 385
QY 359 GACTGAG----AGTCAGAGCTTGAAGAAAGCTTATTTTCCCAACCTCCCCCAGG 414
Db 386 AACTGAAACAAAGCCATGACTTGAAGAAACAATAATTTGTAACCCCTGCTTCTCAGA 445
QY 415 TGCAGTGTGACATTATTTATTTATTAACATCCACAAGA-GATTATTTTAAATAATTAA 473
Db 446 GTGCTTCTGAGATTATTTAAATCTAATTTCTAAGGAATAGAGCTTTATGTAATAATGTA 505
QY 474 AGCATATATTTCTTAAAGATTTAATTATATTTAAGTGTGATGTTTAACTCTAT 533
Db 506 ATCATGTTTCTTAGATTTTAA-----AAGTTATTAATATTTTAAATTTAAT 556
QY 534 CTGTCATACATCTAGTGAATGTAAATGCAAAATCCTGTCATGTTTGTGTTTTG 593
Db 557 CTTCCATGATTTTGTGGGTTTGAACATAAAGCCTTGATGTATATGTCATCTCAGTG 616
QY 594 TTTT 597
Db 617 CTGT 620

RESULT 8
US-10-044-090-494
; Sequence 494, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 494
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 222839.1
US-10-044-090-494

Query Match 27.08; Score 230.8; DB 12; Length 987;
Best Local Similarity 68.08; Pred. No. 5.5e-34;

Matches 400; Conservative 0; Mismatches 172; Indels 16; Gaps 5;

QY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAAGATGAAGTTTCTGCA 60
Db 159 AAACCAACACCTCTCACAGCCAAAGCTCACACCTTCAGCCTCCAACATGAAGTCTCCGCA 218
QY 61 GCGCTTCTGTGCTGCTGCTCATGCGACCACTTTCAGCCCTCAGGAGCTGTGCTCAGCCA 120
Db 219 GCACCTTCTGTGCTGCTGCTCATAGCAGCTGCTTCAGCCCCCAGGGGCTCAGTGCGCA 278
QY 121 GATTACATTTCATTCCAATCACCTGCTGCTTTAAGTGATCAATAGAAATTCCTATC 180
Db 279 GCTTCTG-----TCCCAACCACCTGCTGCTTTAACTGGCCAATAGAAATACCCCTT 332
QY 181 CAGAGCTGGAGAGCTACACAGAATCACCAACATCCATGTCCCAAGGAGCTGTGATC 240
Db 333 CAGGAGCTAGAGAGCTACAGAGAATCACAGTGGCAATGTCCCAAGAAAGCTGTGATC 392
QY 241 TTCAAGACCAAAACGGGCAAGGAGGTCTGCTGACCCCAAGGAGAGATGGGTCAAGGAT 300
Db 393 TTCAAGACCAAACTGGCCAAAGATATCTGTGCCGACCCCAAGAAAGATGGGTGCAAGAT 452
QY 301 TCCATGAAGCATCTGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATG-- 358
Db 453 TCCATGAAGTATCTGACCAAAATATCTCAACTCCAAAGCCATTAATATACCATTTT 512
QY 359 GACTGAGAGCTGAGAGCTTGAAGAAAGCTTATTTTCCCAACCTCCCCCAGGTGCA 418
Db 513 GAAACCAACAGAGAGCTGAGTGTGCCCTTAATTTGTTTC----CCTCTTACAATGCA 567
QY 419 GTGTGACATTATTTTATTAACATCCACAAGAGATTATTTTAAATAATTAAAGCAT 478
Db 568 TTCTGAGGTAAACCTCATATTAT--CAGTCCAAGGGCATGGGTTTATTAATATATATATA 625
QY 479 AATATTTCTTAAAGATTTAATTATTAAGTGTGATGTTTAACTC-TATCTGT 537
Db 626 TTTTAAATAAAAGATATGCAATTAATTATTTGAGGCTTTAAACTATATCCTC 685
QY 538 CATACATCTAGTGAATGTAAATGCAAAATCCTGTCATGTTT 585
Db 686 CATGAATATCAGTTATTTTAAACTGTAAAGCTTTGTGAGATTTCTT 733

RESULT 9
US-08-927-939-76
; Sequence 76, Application US/08927939
; Patent No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Gralinger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(331)
US-08-927-939-76

Query Match 26.68; Score 227.8; DB 8; Length 685;
Best Local Similarity 63.88; Pred. No. 1.8e-33;
Matches 370; Conservative 9; Mismatches 198; Indels 3; Gaps 3;

QY 14 TCATGCTGAAGCTCACACCCCTTGCCCTCAAGATGAAGTTCCTGACGCTTCTGTGCC 73
Db 1 TCAACTGAAGCTCGCACTCTGCC-TCACAGCATGAAGTCTGTGCCCTTCTGTGCC 59

[illegible]

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RESULT 10
US-09-981-876-106
; Sequence 106, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: 70 Human Secreted Proteins
;   FILE REFERENCE: P2001P1
;   CURRENT APPLICATION NUMBER: US/09/981,876
;   CURRENT FILING DATE: 2001-10-19
;   PRIOR APPLICATION NUMBER: 09/148,545
;   PRIOR FILING DATE: 1998-09-04
;   PRIOR APPLICATION NUMBER: 60/040,162
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,333
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/038,621
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,161
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,626
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,334
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,336
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,163
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;; LENGTH: 1712

Query Match 26.0%; Score 222.6; DB 9; Length 1712;
Best Local Similarity 68.3%; Pred. No. 2e-32;
Matches 405; Conservative 1; Mismatches 160; Indels 27; Gaps 6;

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; Sequence 106, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

1	TITLE OF INVENTION: 70 Human Secreted Proteins
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3	CURRENT APPLICATION NUMBER: US/09/148,545
4	CURRENT FILING DATE: 1998-09-04
5	EARLIER APPLICATION NUMBER: PCT/US98/04482
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RESULT 12
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; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
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; CURRENT FILING DATE: 2001-10-19
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; PRIOR APPLICATION NUMBER: 60/040, 161
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; PRIOR APPLICATION NUMBER: 60/040, 626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040, 334
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; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040, 163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047, 615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047, 600
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; PRIOR APPLICATION NUMBER: 60/047, 597
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; PRIOR APPLICATION NUMBER: 60/047, 502
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; PRIOR APPLICATION NUMBER: 60/047, 633
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047, 617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047, 618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047, 503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047, 592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047, 581
; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 1822

Query Match 26.0%; Score 222.6; DB 9; Length 1822;
Best Local Similarity 68.3%; Pred. No. 2e-32;
Matches 405; Conservative 1; Mismatches 160; Indels 27; Gaps 6;

QY 1 AAACCTCAGCTCTCATGCTGAAGCTCACACCTTGCCCTCCAGATGAAGTTTCTGCA 60
Db 1056 AAACATCCAAATTCCTCAAACTGAAGCTCGCACTCTCG-CCTCCAGCATGAAGTCTCTGCC 1114
QY 61 GCGCTTCCTGCTGCTGCTCATGCGCAGCCACTTTACGCCCTCAGGACTTGCTCAGCCA 120
Db 1115 GCGCTTCCTGCTGCTGCTCATGCGCAGCCACTTTATCCCAAGGCTGCTCAGCCA 1174
QY 121 GATTCAGTTTCCATTCCTCAATCACCCTGCTTTAAGCTGATCAATAGGAAAATTCCTATC 180
Db 1175 GATCCAAATCAATGCCCCAGTCACCTGCTGTATTAACCTTCACCAATAGGAAGATCTCAGTG 1234
QY 181 CAGAGGCTGAGAGCTACACAGAATCAGACATCCAATGTCCCAAGAGCTGTGATC 240
Db 1235 CAGAGGCTGCGAGCTATAGAGAATCAGCAGCAAGTGTCCCAAGAGCTGTGATC 1294
QY 241 TTCAAGACCAAAAGGGGCAAGAGAGTCTGTGCTGACCCCAAGAGAGAGATGGTTCAGGGAT 300
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QY 301 TCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCCTTCATACATGGA 360
Db 1355 TCCATGGACCACTGGACCAAGCAAAACCAACTCCGAAGACTTGAACACTGACTCCACAA 1414
QY 361 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTTATTTCCCAACCTCCCCAGGTGCAGT 420
Db 1415 CCCA----AGAACTGCAGCTAA---CTTAATTTCCCTAGCTTTCCCGACACACCCT 1465
QY 421 GTGACATTAATTTATTAATACATCCACAAAGATATTTTAAATAATTTAAAGCATAA 480
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QY 481 TATTTCTTAAAGTATTTATTTATTTAAGTTGTGATGTTTAACCTCATCTGTCAT 540
Db 1510 TATGCCCTTAAGTAAATGTTAATCTTAATTTAAGTTATGATGTTTAAAGTTAATCTTTCAT 1569
QY 541 ACATCCATGATGTAATAATGCAAAATCCTGCTGATGTGTTTTTGTGTTTG 593
Db 1570 GG-TACTAGTGTGTTTATAGATACAGAGACTGGGAAATGCTTTCCCTCTG 1621

RESULT 13

US-09-148-545-105
; Sequence 105, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; EARLIER FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
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EARLIER APPLICATION NUMBER: 60/043,315
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EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/047,595
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EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 05-Sep-1997
EARLIER APPLICATION NUMBER: 60/047,599
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EARLIER APPLICATION NUMBER: 60/047,614
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EARLIER APPLICATION NUMBER: 60/043,578

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EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
LENGTH: 1822

Query Match 26.0%; Score 222.6; DB 9; length 1822;
Best Local Similarity 68.3%; Pred. No. 2e-32;
Matches 405; Conservative 1; Mismatches 160; Indels 27; Gaps 6;

QY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTTGCCCTCCAGATGAAGTTCTGCA 60
DB 1056 AAACATCCAATTCTCAACTGAAGCTCGCACTCTCG-CCCTCAGCATGAAGTCTCTGCC 1114
QY 61 GCGCTCTGTGCGCTGCTCATGCGAGCCACTTTCAGCCCTCAGGGACTGCTCAGCCA 120
DB 1115 GCCCTTCTGTGCTGCTGCATAGCAGCCACCTTCATTCCCAAGGGCTCGCTCAGCCA 1174
QY 121 GATTCAGTTTCCATTCCAATCACTGCTGCTTAAACGTGATCAATAGAAATTCCTATC 180
DB 1175 GATGCAATCAATGCCCCAGTCACTGCTGYTATTAATTACCAATAGGAAGATCTCAGTG 1234
QY 181 CAGAGCTGAGAGCTACACAAGAATCACCAACATCCAATGTCCTCAAGAGCTGTGATC 240
DB 1235 CAGAGGCTCGGAGCTATAGAGAATCACAGCAGCAAGTGTCCCAAGAAGCTGTGATC 1294
QY 241 TTCAAGACCAAAACGGGCAAGAGAGTCTGTGCTGACCCCAAGAGAGATGGTCAAGGAT 300
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QY 301 TCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA 360
DB 1355 TCCATGGAACCACTGGACAGCAAAACCAAACTCCGAAGACTGAACACTCACTCCACAA 1414
QY 361 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTATTTCCTCCCAACTCCCCAGGTGACGT 420
DB 1415 CCGA-----AGATCTGACGTAA-----CTTATTTTCCCTAGCTTCCCCAGACACCCCT 1465
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DB 1466 GTTTTATTATTATATAT-----GAATTTTGTGTGTGATGTGAACAACAT-- 1509
QY 481 TATTTCTTAAAGATATTAAATATATTAAAGTTGTGATGTTTAACTCTATCTGTGAT 540

Db 1510 TATGCCCTTAAGTAATGTTAATCTTATTAAGTTATGTGATGTTTAAAGTTAATCTTCAT 1569
QY 541 ACATCCTAGTGAATGTAAATGCAAAATCCTGCTGATGTGTTTGTGTTTGTG 593
Db 1570 GG-TACTAGTGTGTTTGTAGATACAGAGACTTGGGAAATTGCTTTCCCTCTG 1621

RESULT 14
US-10-044-090-583

; Sequence 583, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 583
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 452327CB1
US-10-044-090-583

Query Match 25.9%; Score 221.4; DB 12; Length 804;
Best Local Similarity 68.3%; Pred. No. 2.8e-32;
Matches 405; Conservative 0; Mismatches 161; Indels 27; Gaps 6;

QY 1 AAACCTTCACCTCTCATGCTGAGCTCACACCTTGCCCTCCACAGATGAAGTTTCTGCA 60
Db 74 AAACATCCAATTCCTCAAACTGAAAGCTCGACTCTCG-CCTCCAGCATGAAGTCTGACC 132
QY 61 GCGCTTCTGTGCTGCTGCTCATGCGACCACTTTCAGCCCTCAGGACTGCTCAGCCA 120
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QY 121 GATTCAGTTTCCATTCCTCAATCACCCTGCTGCTTAAAGTGTATGATCAATAGGAAATTCCTATC 180
Db 193 GATGCAATCAATGCCCCAGTCACCTGCTGTTATACTTCACCAATAGGAGATCTCAGTG 252
QY 181 CAGAGGCTGGAGAGCTACACAGAATCACCAATCCCAATGTCCCAAGAGAGCTGTGATC 240
Db 253 CAGAGGCTGGAGAGCTATAGAGAATCACCAAGCAAGTGTCCCAAGAGAGCTGTGATC 312
QY 241 TTCAAGACCAAAACGGGGCAAGAGGCTGTGCTGACCCCAAGAGAGAGATGGCTCAGGAT 300
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QY 301 TCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCCTTCATACATGA 360
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QY 361 CTGAGAGTCAGAGCTTGAAGAAAAGCTTATTTTCCCAACCTCCCCGAGGTGACGT 420
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QY 421 GTGACATTTATTTATTTATTAACATCCACAAAGATTTATTTTAAATTAATTAAGCATAA 480
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Db 528 TATGCTTAAGTAATGTTAATCTTATTTAAGTATTTGATGTTTAAAGTTATCTTTCAT 587
QY 541 ACATCCTAGTGAATGTAAATGCAAAATCCTGCTGATGTGTTTGTGTTTGTG 593
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RESULT 15
US-10-044-090-822

; Sequence 822, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 822
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 223187CB1
US-10-044-090-822

Query Match 25.6%; Score 218.8; DB 12; Length 600;
Best Local Similarity 75.1%; Pred. No. 7.9e-32;
Matches 302; Conservative 0; Mismatches 92; Indels 8; Gaps 2;

QY 1 AAACCTTCACCTCTCATGCTGAGCTCACACCTTGCCCTCCACAGATGAAGTTTCTGCA 60
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QY 121 GATTCAGTTTCCATTCCTCAATCACCCTGCTGCTTAAAGTGTATGAGAAATTCCTATC 180
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Search completed: February 18, 2003, 03:01:41
Job time : 83 secs